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em_htgo_other:*

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SUMMARIES

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ALIGNMENTS

JOURNAL	TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AX107857	RESULT 1
Patent: WO 0123550-A 1 05-APR-2001;	Pca3 messenger rna species in benign and malignant prostate tissues	Busse, U., Chypre, C. and Fradet, Y.	1	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	Homo sapiens (human)		AX107857.1 GI:13923249	AX107857	Sequence 1 from Patent WO0123550.	AX107857 506 bp DNA linear PAT 30-APR-2001		

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REFERENCE
AUTHORS
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AL359314
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                                                                                                                                           On May 16, 2001 this sequence version replaced gi:13897374. 4/30 of the puring sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
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                        Group. Further information can http://www.sanger.ac.uk/HGP/Chr9 RP11-108L4 is from the library R
                                                                                      http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (15-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
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                                                                   Further information can be found at
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Butheria; Primates; Catarrhini; Hominidae; Homo.
1 to 128480)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
123 c 108 g 14
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For further details see
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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/chromosome="9"
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/mol type="genomic DNA"
                                                                           20399.
                                                                                                                                                                                /note="L1PA2 repeat:
13779. .19033
                                                                                                                                                                                                                                                                                                                           /note="AluSp
10719. .1094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="L2 repeat: matches 2685.
3717. .8827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="AluSq repeat: matches 1. .264 of consensus"
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\827. .1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="MIR repeat: matches 36. .79 of consensus"
       /note="AluSq repeat:
21375. .21414
                                                                                                                                                                                                                      13003.
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                                                        note="MIR repeat:
                                                                                         note="53 copies 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="MLT1F repeat:
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                                                                                                                                                                                                                                                                                                       note="MER58A repeat: matches 1.
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                                                                                                                                                                                                                                                                                                                                          repeat:
                                                                                                                            repeat: matches 136. .230 of consensus"
                                                          matches 112. .146 of consensus"
                                                                                                                                                               matches
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                       matches 1. .310 of consensus"
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37126. .37446
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/note="MLT1B repeat: matches 1.
29408. .29719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="24 copies 2 mer ta 77% conserved" 26946. .27277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="L1MB3 repeat: matches 5736. .6185 of consensus'
25327. .25632
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21979. .22174
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27721. .28015
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22470. .22629
                                                                                                                                                                                                                            12261. .42665
/note="MLT2FA repeat: matches 1.
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 /note="MIR repeat:
57364. .57658
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15473. .45586
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                                                                          'note="MIR repeat:
                                                                                                      note="L2 repeat: matches 2630.
                                                                                                                                                                 note="MER5A repeat:
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                                                                                                                                                                                      Submitted (28-OCT-1998) Urology Research La
Hospital Nijmegen, P.O. Box 9101, Nijmegen
                                                                                                                                                                                                                                  2 (bases 1 to 5435)
Bussemakers,M.J.G., Van Bokhoven
Karthaus,H.F.M., Schalken,J.A.,
Isaacs,W.B.
                                                                                                                                                                                                                                                                                                                                                                              Bussemakers, M.J., van Bokhoven, A., Verhaegh, G.W., Karthaus, H.F., Schalken, J.A., Debruyne, F.M., Ru, N
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 5435)
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59583..59654
/note="36 copies 2 mer tt 65% cor
59658..59977
/note="Lipa7 repeat: matches 580:
61302..61714
                /rpt_type=dispersed 533. ...697
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61785. .62178
                                                                                                         /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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 note="alternative exon
                                             rpt_family="Aluy"
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nalken,J.A., Debruyne,F.M.J., Ru
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Unpuriance
( bases 1 to 224052)

2 (bases 1 to 224052)

2 (bases 1 to 224052)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Birren,B., Linton,L., Nusbaum,C., Bloom,T., Boguslavkiy,L.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Boukhgalter,B., Brown,A., Collins,S., Collymore,A.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Dodge,S.
Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.
                                                                                                                                                                                                                                                                                                                        Mus musculus clone RP24-222013, unordered pieces.
                                                                                                                                              Bukaryota; Metazoa; Chordata; C:
Mammalia; Eutheria; Rodentia; S:
1 (bases 1 to 224052)
Birren,B., Nusbaum,C. and Lande:
Mammaliaculus, clone RP24-222013
                                                                                                                                                                                                                                                          Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                Unpublished
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60; Conservative
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/product="non-coding RNA DD3"
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Example 1 to 224052)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boukhgalter, B., Camaratta, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, D., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Hall, J., Horton, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbe, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamath, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., MacConald, P., Major, J., Maxquis, N., Matthews, C., McCarthy, M., Mewan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Ngyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Strauss, N., Subramanian, A., Tralamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Tasion, J., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (27-MAR-2003) whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 27, 2003 this sequence version replaced gi:24431740. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html http://ftp.genome.washington.edu/RM/RepeatMasker.html Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                                                                        Insert size: 208000; agarose-fp
Insert size: 222052; sum-of-contigs
Quality coverage: 9.4 in Q20 bases; agarose-fp
Quality coverage: 8.8 in Q20 bases; sum-of-contigs
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44731
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/note="assembly_fragment"
48560. .52262
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/note="assembly_fragment"
44731. .46031
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41965. .42641
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57555. .59456
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55392. .57454
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52363. .55291
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="assembly_fragment"
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'note="assembly_fragment'
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166679: contig of 21235
166779: gap of 100 bp
224052: contig of 57273
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41964: gap of 100 bp
42641: contig of 677 bp in length
42741: gap of 100 bp
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is available and the accession number will
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862: contig of 1121 bp in length
862: gap of 100 bp
530: contig of 668 bp in length
730: gap of 100 bp
731: contig of 668 bp in length
731: gap of 100 bp
731: gap of 100 bp
732: contig of 2328 bp in length
733: gap of 100 bp
733: gap of 100 bp
734: contig of 3703 bp in length
735: contig of 3703 bp in length
736: gap of 100 bp
737: gap of 100 bp
738: gap of 100 bp
739: gap of 100 bp
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KEYWORDS
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      CE 2 (bases 1 to 198517)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, U.S., Dodge, S., Cook, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Ginde, S., Gord, S., Goyette, M., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Leboczky, J., Levine, R., Lindblad-Toh, K., Liu, G., Landers, T., Leboczky, J., Levine, R., Lindblad-Toh, K., Liu, G., McCarthy, M., McEwan, P., Major, J., Marquis, N., Meneus, L., Mihova, T., Meloga, V., Muzphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Nicol, R., Mihova, T., Menga, V., Muzphy, T., Naylor, J., Nguyen, C., Nicol, R., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Stauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
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AC115779.5 GI:29294112
AC115779.5 PHASE1; HTGS_DRAFT.
'have mouse)
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Mus musculus clone RP23-153L22,
unordered pieces.
AC11577°
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Birren,B., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-153L22
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/note="assembly_fragment"
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145445. .166679
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65509. .69990
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70091. .73982
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
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Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choe Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faradyna, S., Bogley, R., Bardyna, S., Bard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 19514 bases at least Q40
Consensus quality: 19534 bases at least Q30
Consensus quality: 196343 bases at least Q20
Insert size: 197417; sum-of-contigs
Quality coverage: 10.1 in Q20 bases; sum-of-contigs
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17349: contig of 17349 bp in length
17449: gap of 100 bp
18521: contig of 1072 bp in length
18621: gap of 100 bp
19526: contig of 905 bp in length
19626: gap of 100 bp
21227: contig of 1601 bp in length
21227: contig of 1601 bp
24152: gap of 100 bp
24152: contig of 2825 bp in length
24252: gap of 100 bp
29767: contig of 5815 bp in length
29867: gap of 100 bp
35683: contig of 5816 bp in length
35783: gap of 100 bp
35783: gap of 100 bp
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Direct Submission
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46652: gap of 100 bp

68280: contig of 21628 bp i:

68380: gap of 100 bp

87560: contig of 19180 bp i:

87660: gap of 100 bp

166311: contig of 78651 bp i:

166411: gap of 100 bp

198517: contig of 32106 bp i
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Submitted (23-APR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirrong Bao and Sean Eddy, submitted), and those beginning 'Gr' were identified by The Recon repeat discovery system (Zhirrong Bao and Sean Eddy, submitted), and those beginning 'Gr'
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Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Apr 11, 2003 this sequence version replaced gi:29786465.
                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 177658)
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                                                                                           Submitted (11-APR-2003) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                            Danio rerio
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AL935269
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CH211-117M12 is from a CHORI-211 BAC library
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                                                                                                                              Direct Submission
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/db_xref="taxon:7955"
/clone="CH211-117M12"
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'Orr' were identified by Rick Waterman (Stephen Johnson lab, Washu). For further information see http://www/Projects/D_rerio/fishmask.shtml DECTORD.-InfoRDAG-S
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                                                                                                                                                                                              Diagnocure Inc. (CA)
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Pca3 messenger rna species in benign and malignant prostate tissues
Patent: WO 0123550-A 4 05-APR-2001;
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Contact: zfish-help@sanger.ac.uk
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                                            /note="oligonucleotide"
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Oryza sativa (japonica
PAC clone:P0413C03.
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* NOTE: This is a 'working draft' sequence. It currently * consists of 2 contigs. Gaps between the contigs * are represented as runs of N. The order of the pieces * is believed to be correct as given, however the sizes * of the gaps between them are based on estimates that have
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantas; Streptophyta;
Spermatophyta; Magnoliophyta; Liliopsida
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 153479)
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Oryza sativa (japonica cultivar-group) chromosome 1 clone
OSJNBa0034K07, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.
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Hahn, J.-H. and Eun, M.Y.
Direct Submission
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and Eun, M.Y.
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This sequence will be replaced

This sequence will be replaced

by the finished sequence as soon as it is available

the accession number will be preserved.

1 45287: contig of 45287 bp in length

45288 45387: gap of unknown length

45388 153479: contig of 108092 bp in length.
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33690 c 32999 g 42
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/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
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Liliopsida; Poales; Poaceae;
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6.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP2.0. ESTS represent the identified cDNA sequences using BLASTN 2.0 with the corresponding DDBJ accession no. and RGP clone ID. A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.

The orientation of the sequence is from SP6 to T7 of the PAC clone. This sequence of P0413CO3 clone has an overlap with P0678F11 (DDBJ: AP003437) clone at the position 148,368 to 150,019 of 3' end. The sequence of this clone ends at the position 13,793 of P0678F11. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp/, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
On Mar 12, 2002 this sequence version replaced gi:16904688. Genes were predicted from the integrated results of the following: GENSCANI.0, BLASTNZ.0, BLASTXZ.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against NCBI NonRedundant Protein database, at the County Coun
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Antonio,B.A., Kanamori,H., Hosokawa,S., N
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/db_xref="taxon:39947"
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                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Oryza sativa
mol_type="genomic DNA"
'protein_id="BAB86126.1"
                                                                          note="hypothetical protein"
                                                                                                                 gene="P0413C03.
                                                                                                                                                    oin(1042. .1208,1804. .1858)
                                                                                                                                                                                   gene="P0413C03.1"
                                                                                                                                                                                                                                                             clone="P0413C03"
                                                                                                                                                                                                                                                                                                        chromosome="1"
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SdC

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tränalation="MEQLRTIGRELAMGSQGGWGQSKEFLDLVKSIGEARSKAEEDRI
ISRELDHLKRRLADEDVPRRKWKELLLRLVYAEMLAGHDASFGHLHAVKWTHDESLPKI
RTGYLAVSLFLDERHDLVILVVNITGKDLSSUNTLVVGHDASFGHLHAVKWTHDESLPKLF
RTGYLAVSLFLDERHDLVILVVNITGKDLSSUNTLVVSHFAKLCDNDPGVMGATLCPL
QVVELLAHPKEAVRKKAVMALHRFYQRSPSSVSHLVSNFRKRLCDNDPGVMGATLCPL
TDLILEDDNSYKDLVVSFVNILKQVAERRLFTSYDYHQMPAPFIQIKLLKILAVLGSG
DKQASGNMYMVLGDIRRKEQDTASNIGNALLYEGICICISI FPNAKMLDAAAETTSKFL
KSDSHNLKYMGIDALGRLIKINPDIAEBHQLAVIDCLEDPDDTLKRKTFELLYKMTKS
TNVEVLYVDRMIEYMINITDHHYKTELASRCVELAEQRAPSNOMFIQITGMKVFEHAGDL
VNIRVAHNLHAEGFGEEDEGADSQLRSSAVDSYLLIVGEPKLPSSFLQICWVLG
EYGTADGKYSASYIIGKLYDVAEAHPTDDTVRAYAISAILKIFAFEIALGRKLIDMLPE
CQSLLDELSASHSTDLQQRAYELQALLGLDKGAVENWPADASCEDIFITENSLSFLNG
CQSLLDELSASHSTDLQQRAYELQALLGLDKGAVENWPADASCEDIFITENSLSFLNG
CQSLLDELSASHSTDLQQRAYELQALLGLDKGAVENWPADASCEDIFITENSLSFLNG
CQSLLDELSASHSTDLQQRAYELQALLGLDKGAVENWPADASCEDIFITENSLSFLNG
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CQSLLDELSASHSTDLQQRAYELQALLGLDKGAVENWPADASCEDIFITENSLSFLNG
                                                                                                                                                                                                                                                                                                                                                                                                    RSPWTTSEEYPRYTSDDDNRSGSGSDDDDDHGDRNRRRGKKSNKKKSSSSSSSYKYDD
DGGERDRSYSNYGGYGNNEGYSSSAPSGYNPYNNGGGYGGFSYGNGGGYGGSTYGNGG
GYGGSSYGNGGAIVAGGGGGSAPASYGYGSNSGWGAPAPPRQEGGSGSAPTYLNVIYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="contains EST AU068098(C11856)
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(10814. .11478,13318. .13418,14749. .14934,
15151. .15224))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TQPGSSSSQNENSGERRDNGGGGGGRNGLFGPTFQAVGGYMDRRFGFD" complement (join(10814...11478,13318...13418,14749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="contains ESTs AU100652(C11143),C25923(C11143)
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (7475. .8275)
/gene="P0413C03.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DYQSYTSNNNNNGSDDDKDKNKHKITSSHKHKDDEKDRNNHSKDSHGGGNSSNYNKDS
YGGNSGNPNNYYGSSTGVVAGSGSYYGGGGYGGGNTSYGGSLSYGKDGGYGGSNSPY
GGGSSIIISGAAPIPHNNFGGGGTGWPVPPPPQDGGSGAAPVFIRAEEVKVIYHHTPP
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LQYTILPVDDLTCRSTRYIWPVNTRKLDR"
complement (4165. .5010)
                                                                                                                                                                                                                                                                                                      /product="putative gamma-adaptin 1"
/protein_id="BAB86130.1"
/db_xref="GI:19386749"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FGFHSSD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15151. .15224)
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complement/7---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GHGSSSSSYSPSPKYESEGDRRRSGGAGSGSGSNSGGGGGFFGPAFHAVGGYIDRKF
     YVQQAIENGAAPYIPESERSGVVSVGNYKAQDQQETSAHALRFEAYELPPAASQASIS
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/db_xref="GI:19386747"
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/note="h-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MSWWKKSSGKSSSSSSYYAGSDSSSFAGGGGDDRYGRAGSGNG
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                                                                                                                      Mus musculus
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AC122812.4
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gene

SdS

SdC

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132589 CCACTACCGATTTTCTATTT 132570
1 (bases 1 to 208430)
McPherson, J. D. and Waterston, R. H.
The sequence of Mia minorial.
                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                        AC122812 208430 bp DNA 1
Mus musculus chromosome 1 clone RP23-285M9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCACTACCGATTTTCTATTT 121
   sequence of Mus musculus clone
                                                                                                                                                                                  musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(32933, .33059,33753, .33948,34052, .34279,34608, .34839,
34927, .35034,35147, .35419,35712, .35996)
/gene="P0413C03.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MEGGGGHAPTPGVCRYPAGGSPFAASGRPRICPGGYARLDGKQE EPQERAPSELSCSGSSVDCRRRRNPSLERGGGLEPSEGABPAPPATTPPVI" join (32933. 33059,33753. 33948,34052. 34279,34608. .34839,34927. .35034,35147. .35419,35712. .35996)
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join(28678 . .28714,29296 . .29459,29480 .
/gene="P0413C03.7"
join(28678 . .28714,29296 . .29459,29480 .
/gene="P0413C03.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /traiblation="Moratilihnpeclsltwmlgvhnqirqlmkfptimivqqtlnl
LSKRLFFVNRQAKATIEPTQYGEDLLSNRRNPNALKEHLLKMTAEHRAEMANKRGKPL
HADNGNVEIGNGYGYDFGDKPKDIADKAKGADDLPEFLRQRLARGILKDEATNNRFT
IKQNVDSPVGQIKAAQELPEGWEAKDPTSGASYFYNQSTGTTQWDDRDAFDLNTMQHQ
IKQNVDSPVGQIKAAQELPEGWEAKDPTSGASYFYNQSTGTDWDRYGAPLNTMQHQ
APPSGSSLPEWMEEALDQSTGQKYYYNTNTQATQWEPDTAVNGVAPHAPTNAAVEMAA
QNTDIWNSQMQRCLIGCGWGVGLVQPWGYCNHCTRVQNLPFQQVPSYPNNTTHSSSNK
NPGNVAAKDRSSAKPPFGKANRKDHRKRNRPEDDELDPMDPSSYSDAPRGGWYMIFFI
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27975. .28053,28156. .28234,28437. .28597))
/gene="P0413C03.6"
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similar to Arabidopsis thaliana chromosome
//arabidopsis
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26050. .26215,26559. .26612,26978. .27108,27228. .27269,
27975. .28053,28156. .28234,28437. .28597))
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TQLEGLLGPASASPVVSETPASSTSKTPDLMSIFSDDVQTGVTSGSTEPSLGVNVVAA
KKGPSLQDALQKDAAARQVGVTPTGNNPILFKDLLG"
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SSSTSSQQATNGGVSSEVGGSTSSQARESTYGSKRQQATEVSAEKQRLAASLFGKADR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="putative selenium binding protein"
/protein_id="BAB86133.1"
/db_xref="GI:19386752"
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/db_xref="GI:19386750"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MAAAANGAACCGGATGPGYATPLEAMEKGPREKLLYVTCVYNGT/
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/gene="P0413C03.8"
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Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalbechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, B., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davas, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Bgan, A., Escotto, M., Sugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
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On Sep 6
                                                                                                                                                                                                                                                                                                                                                                                                                                HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ENRICHED Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC109025 215616 bp DNA Rattus norvegicus clone CH230-276A24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (06-SEP-2002) Genome Sequencing Center, 4444 Forest Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 208430)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (25-AUG-2002) Genome Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 (bases 1 to 208430)
McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (25-MAY-2002) Genome Sequencing Center, 4444 Forest Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 208430) McPherson, J.D. and Wat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: M_BA0285M09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC109025.5 GI:25139227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC109025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site:http://genome.wustl.edu/gsc/index.shtml
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                                                                                                                                                                                                                                                                                                                                      (bases 1 to 215616)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="1"
/clone="RP23-285M9"
a 40063 c 41477 g 65247 t
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,, 2002 this sequence version replaced gi:22475552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.8%; Score 20;
100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Center -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG 20-NOV-2002
IN PROGRESS
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TITLE JOURNAL REFERENCE

AUTHORS TITLE

JOURNAL

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

Center project name: GPRH Center clone name: CH230-276A24 Center Summary Statistics Assembly program: Phrap; version 0.990329 Consensus quality: 181529 bases at least Q40 Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu

Project Information

Center: Baylor College Center code: BCM

of Medicine

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Graer, C.M., Gabisi, A., Ganta, R., Garcia, A., Garrer, T., Garra, M., Gebregeorys, E. B., Geer, K., Gill, R., Gardy, W., Gerran, G., Gerr
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FEATURES

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REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                      AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                  Mus musculus chromosome UNK clone RP24-234J3, WORKING DRAFT SEQUENCE, 11 unordered pieces.
AC132315
AC132315.1 GI:22657777
AC132315.1 GI:22657777
HTG; PHASEL; HTGS_DRAFT; HTGS_FULLTOP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
Submitted (03-SEP-2002) Genome Sequencing Center, 4444 Forest Park
                                                             2 (bases 1 to 230279) McPherson, J.D. and Wat
                                   Direct Submission
                                                                                                                                                                                 1 (bases 1 to 230279)
McPherson, J.D. and Wat
                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                       The sequence of Mus musculus clone Unpublished
                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC132315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 215616: contig of 215616 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGTGCTTTATAAAGCACTC 30565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGTGCTTTATAAAGCACTC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    end_sequence:BZ161263"
52149 a 44056 c 42561 g 47
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NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Consensus quality: 183677 bases at least Q30 consensus quality: 185417 bases at least Q20 Estimated insert size: 187302; sum-of-contigs estimation Quality coverage: 6x in Q20 bases; sum-of-contigs estimated.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="wgs_contig"
complement(212205.
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114,05. .12230
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clone_end:Sp6"
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clone_end:Sp6"
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/mol_type="genomic DNA"

/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .1067
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100.0%; Pr/
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                                                                                                                                                                                    and Waterston, R.H.
                                                             and Waterston, R.H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230279 bp
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                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: M13; 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert size: 196000; agarose-fp
Insert size: 228189; sum-of-contigs
Quality coverage: 17.24 in Q20 bases; agarose-fp
Quality coverage: 11.34 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: M_BB0234J03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: WUGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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59107
59207
88463
88563
134958
135058
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32165
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                                                                                                                                                                                                                                                                                                               /note="assembly_name:Contig11"
372. .1190
                      13017. .32164
/note="assembly_name:Contig22"
                                                                                /note="assembly_name:Contig21"
                                                                                                                                                    /note="assembly_name:Contig20"
                                                                                                                                                                                                                                                 /note="assembly_name:Contig14"
1291. .2555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation
                                                                                                                                                                                                                 note="assembly_name:Contig16"
                                                                                                                                                                                                                                                                                                                                                                                                         clone="RP24-234J3"
                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosome="UNK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59206: gap of unknown length
88462: contig of 29256 bp in 1
88562: gap of unknown length
134957: contig of 46395 bp in 1
135057: gap of unknown length
170399: contig of 35342 bp in 1
170499: gap of unknown length
230279: contig of 59780 bp in 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2655: gap of unknown length
4166: contig of 1531 bp in length
4286: gap of unknown length
12916: contig of 8630 bp in length
13016: gap of unknown length
32164: contig of 19148 bp in length
52164: gap of unknown length
59106: contig of 26842 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _xref="genomic DNA"
                                                                                                                                 .12916
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gap of unknown length
contig of 1265 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig of 271 bp in length gap of unknown length
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VERSION KEYWORDS

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AC141860/c
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The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Akhter.N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Boutfard, G.G., Brinkley, C., Brooks, S. Cariaga, K., Coleman, B., Engle, J., Granite, S., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Haric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, B.H., Masiello, C., Maskeri, B., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Paguirigan, C., Pearson, R., Schueler, M.G., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L., Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTG; HTGS PHASE2; HTGS DRAFT Gallus gallus (chicken)
Gallus gallus
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                                                                                                                                                                                                                                                                                                                                 Submitted (03-APR-2003) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Apr 3, 2003 this sequence version replaced gi:29124110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Green, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (19-MAR-2003) NIH Intramural Sequencing
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 237234)
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                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Green, E.D.
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                                                                                                                                                                                               Center project name: dft
Center clone name: 057D10
                                                                                                                                                                                                                                                                      Center: NIH Intramural Sequencing Center Center code: NISC
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88563. .134957
/note="assembly_name:Contig25"
135058. .170399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_name:Contig23" 59207. .88462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_name:Contig26"
170500. .230279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_name:Contig27"
53964 c 52004 g 59749 t
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Pred. No.
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* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

1 12817: contig of 12817 bp in length

* 12918 85073: gap of unknown length

* 85074 85173: gap of unknown length

* 85074 85173: gap of unknown length

* 85174 88714: contig of 3541 bp in length

* 88715 13328: contig of 25114 bp in length

* 88715 13328: contig of 55141 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 consists of 10 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191668
191768
200290
200390
211977
2112077
214146
214246
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114029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insert size: 180000; agarose-fp
Insert size: 236334; sum-of-contigs
Quality coverage: 11.59x in Q20 bases; agarose-fp
Quality coverage: 8.83x in Q20 bases; sum-of-conti
/note="assembly_fragment"
212077. .214145
                                                                                                                                                                                                                                                                                                                          vector_side:left"
12918. .85073
                                                        200390
                                                                                                                                                                                                                     88815.
                                                                                                                                                                                                                                                                                                                                                                                  clone_end:T7
                                                                                                                                                             /note="assembly_fragment"
114029. .191667
                                                                                                                                                                                                                                   /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                     /note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic_DN
/db_xref="taxon:9031"
/clone="TAM31-57D16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                          191768. .200289
                                                                                                                              note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone_
                                                                      note="assembly_fragment"
                                                                                                                                                                                                                                                                                                note="assembly_fragment"
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191667: contig of 77639 bp in length
191767: gap of unknown length
200289: contig of 8522 bp in length
200389: gap of unknown length
211976: contig of 11587 bp in length
212076: gap of unknown length
212076: gap of unknown length
214145: contig of 2069 bp in length
214245: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .237234

    Summary Statistics

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224294: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                lib="TAM31"
                                                                                                                                                                                                                       .113928
                                                                                                                                                                                                                                                                             .88714
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/note="assembly_fragment"

'note="assembly_fragment"

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AC134221/c
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RS Muzny, D. Marie, Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnatead, M., Banhmed, F., Biswalo, K., Blair, J., Blahkenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chen, S., Chen, G., Chen, G., Chen, C., Chen, J., Chen, Z., Chu, J., Cheyle, M., Cree, A., D'Souza, I., Calderon, D., Davila, M.L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Daval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Ferraer, C.M., Gabisi, A., Ganta, R., Garcia, A., Garrer, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, M., Gebregeorgis, E., Geer, K., Handl, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, J., Hune, J., Jahas, H., Johnson, B., Johnson, B., Johnson, B., Johnson, B., Johnson, M., Johnson, R., Johnson, B., Johnson, B., Johnson, B., Johnson, M., Martin, K., Mangum, B., Mapus, P., Martin, K., Martin, R., Poider, A., Steten, M., Oliroz, J., Rehlin, J., Rehter, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapus, P., Martin, K., Martin, R., Martin, S., Parks, K., Pasce, A., Peas, R., Reigh, R., Reigh, R., Reilly, S., Kelly, S., Kelly, S., Martin, R., Martin, R., Martin, S., Parks, K., Pasce, A., Soderger, B., Song, X.-S., Socett, G., Shatsman, S., Shen, H., Valas, R., Valas, R., Villasan, D., Waldron, L., Walker, B., Wang, T., Steen, H., Sosa, J., Wang, J., Wang, J., Wang, J., Wang, J., Waldron, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 GTTTCTATCCTTCCTACTCA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus clone CH230-1005, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Norway rat)
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vector_side:right"
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; Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>,</u>
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AUTHORS
                                                                                                                                                                                                                                                                                                                                               FEATURES
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On Nov 13, 2002 this sequence version replaced gi:23306103.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (24-SEP-2002) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 238817)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu.J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Y., F., Zhang, J., Zhou, J., Zhou, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: Bstimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Caps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         be preserved.
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Consensus quality: 221775 bases at least Q40
Consensus quality: 224525 bases at least Q30
Consensus quality: 226515 bases at least Q30
Consensus quality: 226515 bases at least Q20
Estimated insert size: 226851; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center clone name: CH230-1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                               135351
                                                                                                                                                                                                                                                                                                                                                                                                                   135251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: GDUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center:
                                                                                                                                     /clone="CH230-1005"
87008. .89104
                                                                135351.
                                                                                                                                                                                           /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/note="wgs_contig"
139028. .141263
                                                                /note="wgs_contig"
135351. .136555
                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
                                                                                                                                                                                                                                                                                                              .238817
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                                                                                                                                                                                                                                                                                                                                                                        135250: contig of 135250 bp in length 135350: gap of unknown length 238817: contig of 103467 bp in length
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                                                                                                                                                                                                                                                                                                                                                                            in length.
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ORIGIN
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Best Local Similarity
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Drager, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Eggan, A., Becotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Hernandez, C., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hellins, B., Howells, S., Hulyk, S., Hume, J., Idebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, B., Johnson, R., Jolivet, A., Kargathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Li, Z., Liu, J., Lonlseged, H., Lozado, R.J., Lu, X., Ma, J., Manbuda, P., Martin, R., Martinez, E., Mangum, B., Mapua, P., Martin, K., Marrin, R., Martinez, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Nankervis, C., Newlon, N., Nguyen, N., Norris, S., Nwaokelemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Puzzo, M., Olivez, J., Rachiln, E., Reeves, K., Regier, M., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Raves, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Shenty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Warren, R., Wei, X., White, F., Wan, J., Zhou, X., Zhao, S., Dunn, D., Von, L., Wang, J., Zhou, X., Zhao, S., Dunn, D., Von, L., Wang, J., Zhou, X., Zhao, S., Dunn, D., Von, L., Wang, J., Zhou, X., Zhao, S., Dunn, D., Von, L., Von, V., Zhao, S., Dunn, D., Von, D., Von, V., Zhao, S., Dunn, D., Von, V., Yoon, V.,
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Baldwin, D., Bandaranaike, D., Barber, M., Barnatead, M., Benahmed, F.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Bryant, N., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, P., Souza, L.,
Cleveland, C., Cokrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Press, M., Carter, A., Divya, K.,
Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Press, C., Charles, C., Ding, Y., Dinh, H., Divya, K.,
Press, C., Charles, C., Cha
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Rattus norvegicus (Norway rat)
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Rattus norvegicus clone CH230-93J21, WORKING DRAFT SEQUENCE.
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Allen,C., Allen,H., Alsbrooks,S
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Rodentia;
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Pred. No.
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submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 10, 2003 this sequence version replaced gi:23264500. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 provided by the submittor.

This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

1 243174: contig of 243174 bp in length.
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NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
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Cenome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: GGXU
Center clone name: CH220-93U21
Center clone name: CH220-93U21
Center clone name: CH220-93U21
Consembly program: Atlas 3.0;
Consensus quality: 234402 bases at least Q40
Consensus quality: 236580 bases at least Q30
Consensus quality: 236580 bases at least Q30
Consensus quality: 237637 bases at least Q20
Estimated insert size: 243918; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
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Center code: BCM
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end_sequence:BH327070"
complement(240473...24
                                                                            site: EcoR
                                                                                                                      clone
                                                                                                                                                                                                                            /note="wgs_end_extension
clone_end:T7"
                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA
/db_xref="taxon:10116"
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/mol_type="genomic DNA"
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McPherson, J.D. and Wat
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                        Parkway, St. Louis, MO 63108, USA On Oct 17, 2002 this sequence version replaced gi:23683310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (23-MAY-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
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McPherson, J.D. and Wat
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                                                           20;
                                                                                                                                                                                                                                                                                                               Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (17-OCT-2002) Genome Sequencing Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (10-OCT-2002) Genome Sequencing Center, Parkway, St. Louis, MO 63108, USA 4 (bases 1 to 247309) McPherson,J.D. and Waterston,R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 (bases 1 to 247309)
McPherson, J.D. and Wat
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Mammalia; Eutheria; Rodentia;
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AC122189.4 GI:24080766
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Mus musculus chromosome
                                                                                                                                                                                                                                                          Center project name: M_BA0036C08
                                                                                                                                                                                                                                                                                     Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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Unpublished
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larity 100.0%;
Conservative
                                                                                                                           /organism="Mus musculus"
/mol type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="11"
/clone="RP23-36C8"
a 47853 c 48954 g 77992
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                                                                                                                                                                                                                                                                                                                                                                                                           Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan (E-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Osada, N., Hida, M., Kusuda, J., Tanuma, R., Iseki, K., Hirai, M., Terao, K., Suzuki, Y., Sugano, S. and Hashimoto, K. Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fis (full insert sequence).
Macaca fascicularis (crab-eating macaque)
Macaca fascicularis
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Macaca fascicularis brain cDNA,
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19; Conserv
           genome.
AE010268 AE009950
AE010268.1 GI:18893862
                                                       Pyrococcus
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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                                                                                                                                                                                                                                                               /tissue_type="brain p
/clone_lib="macaque b
/dev_stage="adult"
a 321 c 402 g
                                                                                                                                                                                                                                                                                                                                                    /organism="Macaca fascicularis"
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                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                        sex="male"
                                                                                                                                                                                                                                                                                                                                  clone="QnpA-19858"
                                                       furiosus DSM
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brain cDNA lib
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clone:QnpA-19858.
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SOURCE

Pyrococcus furiosus DSM 3638

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Divergence of the hyperthermophilic archaea Pyrococcus furiosus P. horikoshii inferred from complete genomic sequences
Genetics 152 (4), 1299-1305 (1999)
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Robb.F.T., Maeder,D.L., Brown,J.R., DiRuggiero,J., Stump,M.D.,
Yeh,R.K., Weiss,R.B. and Dunn,D.M.
Genomic sequence of hyperthermophile, Pyrococcus furiosus:
implications for physiology and enzymology
meth. Enzymol. 330, 134-157 (2001)
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Archaea; Euryarchaeota; Thermococci; Thermococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (12-FEB-2002) Human Genetics, University of Utah, South 2030 East, Salt Lake City, UT 84112, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 (bases 1 to 10084)
Weiss, R.B., Dunn, D.M.,
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cus furiosus
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TIYGKAVLNDGPRFIEEVIRRSREEIAEFLKSIDSVNVHELSKKVSREEIERAYEKFY
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YEWSDVMILASTIDNIKAQIRELREISLSNPKDIMIFDIATFKKDVLTEYQGFPREVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="prephenate dehydrogenase"
/protein_id="AAL81827.1"
/db_xref="GI:18893866"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/transl_table=11
                                                                                                 /transl table=11
/product="tryptophan synthase, subunit beta"
/protein_id="AAL81830.1"
/db_xref="GI:18893869"
                                                                                                                                                                                                                                                                                                                                                                               complement (3883. .5049)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="tryptophan synthetase alpha subunit"
/protein_id="AAL81829.1"
/db_xref="GI:18893868"
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/transl_table=11
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            LKDAINEALRDWVATFEYTHYLIGSVVGPHPYPTIVRDFQSVIGREAKAQILEAEGQI
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/transl_table=
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note="Function Code: 1.2 Amino Acid Biosynthesis:
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'gene="PF1703"
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                                                                                                                                                                                                                                                                                                                                                        'gene="PF1706"
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DEFINITION
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Matches 19
                      AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                              7302
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                                                                                                                                   HTG; HTGS_PHASE2.

Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Submitted (03-NOV-1999) Celera Genomics,
                                                                Neoptera; Endopterygota; Diptera; Brachycera; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 13588)
                                                                                                                                                                                                                                 AC012804
AC012804.1 GI:6223516
                                                                                                                                                                                                                                                                                Drosophila melanogaster,
                        Direct Submission
                                       Adams, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                         AC012804
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SLIRHDGKGVYRGLDNPFLAGRYHSLAVLEPPKGFKVTSVSLDDGVIMGIRHKTLPIE
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Aromatic amino acid family; (trpF)"
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MLSYFLQDEEGQIKPTHSIAPGLDYPGVGPEHAYLKKIQRAEYVTVTDEEALKAFHEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="anthranilate synthase
/protein_id="AAL81833.1"
/db_xref="GI:18893872"
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/protein_id="AAL81832.1"
/db_xref="GI:18893871"
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/romatic amino acid family; (trpG)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (5662. .6228)
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/protein id="AAL81831.1"
/db_xref="GI:18893870"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MLIKELDRVSPLRLYLILRQLEYPFILMSAEKHSKKARFTYLSA"
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note="Function Code: 1.2 Amino"
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AC068031
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Best Local Similarity
Matches 19; Conserv
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                                                                                                                                                                                                                                                    Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Mardonald, P., Marquis, N., McCerthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McIdrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T. M., Oliver, J., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vanng, G., Zainoun, J., Zimmer, A., and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rockville, MD, USA
This sequence was identified as CDM:10210414
                                                                                           Research, 320 Charles Street, Cambridge, MA 02141, US All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                    Direct Submission

Submitted (27-APR-2000) Whitehead Institute/MIT Center

Submitted (27-APR-2000) Whitehead Institute/MIT Center
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                         Direct Submission
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                      Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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/mol type="genomic DNA"
/db xref="taxon:7227"
2978 c 2787 g 3921 t
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                                                                           -- Genome Center
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NOTE: This record contains 65 individual sequencing reads that have not been assembled into contige. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
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TITLE
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                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cambridgeshire, CB10 ISA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@ganger.ac.uk
On Nov 15, 2001 this sequence version replaced gi:16304689.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; Sw:,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocal
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                                                                                                                                                                                                                                                                                                                                                    http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr13 RP11-346L13 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                             IMPORTANT: This sequence is not the entire insert of clone RP11-346L13 It may be shorter because we sequence overlappi sections only once, except for a short overlap. The true left end of clone RP11-471M10 is at 68947 in this sequence. The true right end of clone RP11-181D10 is at 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISSPROT; Tr:, TREMBL; \mathtt{Wp}:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human DNA sequence from clone RP11-346L13 on 13q14.3-21.31, complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (14-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                           http://www.chori.org/bacpac/home.htm
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/organism≈"Homo sapiens"
/mol_type="genomic DNA"
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/clone="RP11-360N22"
/clone_lib="RPCI-11 Human Male BAC"
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2 (bases) to 146952)

RS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,

RS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,

Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,

Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,

Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,

Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,

Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,

Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,

Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,

Galagan,J., Gardyna,S., Ginde,S., Jones,C., Kann,L.,

Galagan,J., Gardyna,S., Jones,C., Kann,L., Karatas,A.,

Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J.,

Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,

McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,

Meddrim,J., Meneus,L., Mihova,T., Miranda,C., Menga,V., Morrow,J.,

Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,

O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N.,

Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,

Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,

Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,

Pireft, Submission,J., Zimmer,A. and Zody,M.,

Direct Submission,J., Zimmer,A. and Zody,M.,
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                      Birren, B., Linton, L., Nusbaum, C., I
Anderson, S., Barna, N., Bastien, V.,
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
                                                                         Submitted (03-MAY-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 146952)
                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 146952)
Birren,B., Linton,L., Nusbaum,C.
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HTG.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
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Restriction digest data confirm the assembly."
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/note="Single clone region.
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/note="Single clone region. Sequence from reads from a short insert library derived from a single pUC clone. Restriction digest data confirm the assembly."
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3097. .3326
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/clone="RP11-346L13"
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/chromosome="13"
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25;
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A (bases 1 to 146552)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cock, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Perreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phukhkang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Fieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Ve, M.J., Vonng, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (30-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 30, 2002 this sequence version replaced gi:20331012. All repeats were identified using RepeatMasker: All F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                       Center clone name: 23_K_11
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: L7815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code: WIBR
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/clone="RP11-23K11"
/clone_lib="RPCI-11 Human M.
complement (255. .413)
/rpt_family="MIR"
417. .474
                                                                                                                                                                                                                              organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                              map="8"
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                              /rpt_family="THE18-int"
complement(24454. .2476)
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/rpt_family="L2"
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/rpt_family="L2"
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/rpt_family="Alusx"
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. .4596
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1. .23510
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lement(12690. .12
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Tement(2397. .2
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                                                                                                                                                                                         family="AT_rich"
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                                                                                    Group, Further IIILLINGS, Group, Further IIILLINGS, Group, Further at the Roswell RP3-520B18 is from the library RPCI-3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSJ520B18 148385 bp DNA linear PRI 31-JUL-20 HUMAN DNA sequence from clone RP3-520B18 on chromosome 6p24.1-25. Contains the 5' end of FARSI (phenylalanine-tRNA synthetase), a pseudogene similar to microtubule-associated protein 1A/IB light chain 3, a CpG island, ESTs, STSs and GSSs, complete sequence.
                                                                                                                                                                                                                   The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw:, SWISSROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group, Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      requests: clonerequest@sanger.ac.uk
On Jun 4, 2000 this sequence version replaced gi:8247028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (27-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL121978.5 GI:8247628
HTG; CpG island; tRNA synthetase.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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complement(26647..26752)
/rpt_family="L2"
27726..27924
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26619. .26646
/organism="Homo sapiens"
/mol_type="genomic DNA"
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100.0%; Pred. No. 24.
tive 0; Mismatches
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/note="L2
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1980. 2628
/note="L1PA8 repeat: matches 5514. .6163 of consensus"
/note="L2 repeat: matches 1545.
complement(21298. .21740)
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/chromosome="6"
                                                                                                                                                                                                                                                                      /note="MER47A repeat: matches 2. .366 of
19573. .19646
| note="37 copies 2 mer at 83% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="AluSq repeat: matches 1.
17250. .17555
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                                                                                                      'note="MIR repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="MIR repeat: matches 131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="match: STS:
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                                                                                                                                                                                     note="L2 repeat: matches 2178. .
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                                                                                                    matches 15.
                                                                                                                                                Em: AQ808524"
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                                                               Em: B95444"
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                                                /note="21 copies 2 mer aa 81% conserved" complement (44030. . 44549) /note="match: STS: Em:GS196 match: GSS: Em:AQ585941".
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="match: GSS: Em:AQ133010"
38414. .38743
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29670. .29940
                                  complement (44282. .44623)
                                                                                                                    /note="MIR repeat: matches 69. .122
complement (41352. .41722)
                                                                                                                                                                                                                                                                                                                                                                                        39288. .39581
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complement(37945. .38333)
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                                                                                                                                                                    'note="L1PA5 repeat: matches 4420.
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4981. .36185
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note="MIR repeat: matches 189. .250 of consensus"
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                                                                                                                                                                                      2254. .43416
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2006. .32327
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Homo sapiens chromosome 5 clone
AC093533 AC011082
AC093533.2 GI:29251577
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Submitted (31-AUG-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 154814)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Direct Submission
Submitted (26-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
                                                                                                                                                                              l Similarity
19; Conserv
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On or before Mar 26, 2003 this sequence version replaced
gi:6006258, gi:15383822.
Draft Sequence Produced by DOE Joint Genome Institute
                                            AC016174
                                                                                                                                                                                                                                                                                                                                                       Quality: Phrap Quality >=40 100% of
Estimated Total Number of Errors is
Location/Qualifiers
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DOE Joint Genome Institute and Stanford
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46044. .46305
/note="Alusg repeat: matches 39. .300
46439. .46658
                                                                                                                                                                                                                                                      /clone="RP11-46C20"
26529 c 26123 g
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
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                             161304 bp DNA clone RP11-20K23, WORKING
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Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D.,
Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,
McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,
Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (33-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Mar 16, 2000 this sequence version replaced gi:6721350. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapies, clone RP11-20K23
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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1 (bases 1 to 161304)
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                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: L3921

Center clone name: 20 K 23

Center clone name: 20 K 23

Center clone name: 20 K 23

Sequencing vector: M13, M7915; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.96731

Consensus quality: 148819 bases at least Q40

Consensus quality: 154100 bases at least Q30

Consensus quality: 156644 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert size: 135000; agarose-fp
Insert size: 159504; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www-seq.wi.mit.edu
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1327: gap of 100 bp

3446: contig of 2119 bp i

3546: gap of 100 bp

5141: contig of 1595 bp i

5241: gap of 100 bp

7279: contig of 2038 bp i

7379: gap of 100 bp

9749: contig of 3370 bp i

9849: gap of 100 bp
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|29974. .161304
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                   During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 10); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP, Information on the WORMPEP database can be found at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (25-APR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Apr 26, 2003 this sequence version replaced gi:30024500.
                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/C_elegans/wormpep Repeat names beginning 'Dr' were identified by the Recon repeat discovery syst (Zhirong Bao and Sean Eddy, submitted), and those beginning 'dr' were identified by Rick Waterman (Stephen Johnson lab, WashU). F
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1 (bases 1 to 162939)
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                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml
is from a Zebrafish BAC library
                                                                                                                                                                                                                                                                                  further information see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.sanger.ac.uk
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'db_xref="taxon:7955"
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Levy, A. and Kozlowicz, A.
The sequence of Homo sapiens
Unpublished (2001)
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19; Conserv
                                                                                                        Submitted (23-FEB-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6 On Feb 16, 2002 this seguence version replaced gi:18308807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 164396)
Sulston,J.E. and Waterston,R.
                                                                                                                                                                                                                        Submitted (16-FEB-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                      MO 63108, USA
4 (bases 1 to 164396)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                   Submitted (24-JAN-2002) Genome University School of Medicine,
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Waterston, R.H.
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                                                                                                                                                                                         (bases 1 to 164396)
              Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_NH0137J16
                                                             Center: Washington University Genome Sequencing Center Center code: WUGSC
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by

MAPPING INFORMATION: Mapping information for this clone was provided by \mathtt{Dr} . John \mathtt{D} .

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FEATURES

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Actual start of this clone is at base position 1 of RP11-137J16;
actual end is at base position 164396 of RP11-137J16.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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13995. .14472
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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15370. .15449
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[433. .21764
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7. .23957
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REFERENCE
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AC116849
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                                                                                                                                                                                                                                       Research, 340 Charles

(Dases I to 176785)

RS Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,

Anderson,S., Arachchi,H.M., Barria,N., Bastian,V., Bloom,T.,

Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,

Collymore,A., Cooke,P., Corum,B., DeArellano,K.,

Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,

Ferreira,P., FitzGerald,M., Gaege,D., Galagan,J., Gardyna,S.,

Graham,L., Grand-Pierre,N., Hafges,N., Hagogian,D., Hagos,B.,

Graham,L., Karatas,A., Kells,C., Lilev,I., Johnson,R., Jones,C.,

Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,

Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,

Meldrim,J., Meneus,L., Mihova,T., Mlangs,V., Murphy,T., Naylor,J.,

Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,

O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,

Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,

Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,

Spencer,B., Stange-Thomann,N., Stoyanovic,N., Stubbes,M.,

Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,

Vassillev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,

Mvman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Katatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacChean, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., Marquis, N., Mathews, C., Norchu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Royavo, C., Nurphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Royavo, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Riley, R., Riee, C., Rogov, P., Romann, J., Rosetti, M., Roy, A., Santos, R., Schauser, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stojanow, K., Travere, M., Tralmas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Pire, Submission, T., Zimmer, A., and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (02-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 176785)
Birren,B., Nusbaum,C. and Land
musculus, clone RP24-395F1
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus clone
                                                                                                             Submitted (22-FBB-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 22, 2003 this sequence version replaced gi:20800351.
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Mus musculus (house mouse)
                                    All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176785 bp
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DRAFT SEQUENCE, 13 unordered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as soon as it is available and be preserved.
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Sequencing vector: Plasmid; n/a; 100% of read chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.960731

Consensus quality: 173096 bases at least 040 Consensus quality: 174668 bases at least 020 Consensus quality: 175223 bases at least 020 Consensus quality: 17523 bases at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert size: 168000; agarose-fp
Insert size: 175585; sum-of-contigs
Quality coverage: 8.9 in Q20 bases; agarose-fp
Quality coverage: 8.5 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L25615
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116540
154763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Whitehead
Center code: WIBR
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89775
                                                               /note="assembly_fragment"
91745. .92427
                                                                                                                                  /note="assembly_fragment"
90729. .91644
                                                                                                                                                                                               /note="assembly_fragment"
89875. .90628
                                                                                                                                                                                                                                                                                  vector_side:left"
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                                                                                                                                                                                                                                                                  89055.
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      note="assembly_fragment'
02528. .93177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="RP24-395F1"
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154762: contig of 38223 bp in length
154862: gap of 100 bp
176785: contig of 21923 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          type="genomic DNA"
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89054: gap of 100 bp
89774: contig of 720 bp
89874: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                               lib="RPCI-24 Male Mouse BAC"
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contig of 683 l
gap of 100 bp
contig of 650 l
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gap of 100 bp
contig of 2157 bp in length
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Submitted (21-MAY-2002) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
On Aug 21, 2002 this sequence version replaced gi:21280404.
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2 (bases 1 to 186978)

2 Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
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                                                                                                                    Submitted (08-JAN-2003) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                 Submitted (07-JUN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 192409)
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Center: Baylor College of Medicine
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.h NOTE: This is a "working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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Chemistry: Dye-primer Bodipy: 5% of reads
Chemistry: Dye-primer Bodipy: 95% of reads
Chemistry: Dye-terminator Big Dye: 95% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 171549 bases at least Q40
Consensus quality: 181986 bases at least Q30
Consensus quality: 18593 bases at least Q20
Consensus quality: 18593 bases at least Q20
Estimated insert size: 208123; sum-of-contigs estimation
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Center project name: HBMC
Center clone name: RP11-466116
Summary Statistics
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Contact: hgsc-help@bcm.tmc.edu
----- Project Information
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RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Rafter, B., Earna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Canarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Gonde, S., Gord, S., Goyette, M., Graham, L., Grande Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Jones, C., Kanders, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKerran, K., McPheeters, R., Meldrim, J., McCarthy, M., McEwan, P., McKerran, K., McPheeters, R., Weldrim, J., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Reterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Trigilio, J., Tesfaye, S., Travers, M., Travers, M., Travis, N., Trigilio, J., Va, Wilson, B., Wu, X., Wyman, D., Ye, W. J., Vanssillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Direct Submission
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Submitted (20-UUL-2001) Whitehead Institute/MIT Center for Genomers of Charles Street, Cambridge, MA 02141, USA 1 (bases 1 to 201886)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkly,L., Boukhgalter,B., Brown,A., Changarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens chromosome 8, Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Primates; Ca
1 (bases 1 to 201886)
Birren,B., Linton,L., Nusbaum,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="3"
/clone="RP11-466116"
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128916: contig of 14716 bp in 1.
129016: gap of unknown length
146607: contig of 17591 bp in 1.
146707: gap of unknown length
166353: contig of 19646 bp in 1.
166453: gap of unknown length
16453: gap of unknown length
192409: contig of 25956 bp in 1.
vcation/Qualifiers
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Pred. No.
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Ne 8, clone RP11-661A3, complete sequence.
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                                                                                                                                                                                Center project Information

Center project name: H NH0661A03

Sequencing vector: Summary Statistics

Sequencing vector: M13; 100%

Chemistry: Dye-terminator Big Dye; 8% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 192742 bases at least Q40

Consensus quality: 19476 bases at least Q30

Consensus quality: 196287 bases at least Q20

Insert size: 199083; sum-of-contigs

Quality coverage: 4.81 in Q20 bases; sgarose-fp

Quality coverage: 4.81 in Q20 bases; sgarose-fp

Quality coverage: 4.95 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 ATTTTCTATTTCTTGCCTC 129
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19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (28-FEB-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Apr 21, 2000 this serveror .....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 202983)
Waterston, R. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC024249
AC024249.3 GI:7631100
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site:http://genome.wustl.edu/gsc/index.shtml
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Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence of Homo sapiens clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens chromosome
                                   NOTE: This is a 'working draft' sequence. It currently consists of 40 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
   be preserved
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/rpt_family="(TATG)n"
45409. .45463
/rpt_family="MLT2D"
complement(45464. .45891)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="AluSx"
complement(44323. .44921)
/rpt_family="L1"
44923. .45311
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100.0%;
1100: contig of 1100 bp in length
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Pred. No.
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He 8 clone RP11-661A3, WORKING
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DRAFT SEQUENCE,
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17876: gap of
20852: gap of
20952: gap of
22955: gap of
22905: gap of
22905: gap of
24830: gap of
24830: gap of
26998: gap of
26998: gap of
29838: contig
29938: gap of
33455: gap of
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   Gap of Ga
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g of 1197 bg
f unknown len
g of 1431 bp
g of 1682 bp
g of 1682 bp
f unknown len
g of 1444 bp
g of 1368 bp
g of 1368 bp
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ACCESSION VERSION KEYWORDS

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                             clone_end:SP6
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15543. .17776
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1201. .2689
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/chromosome="8"
                                                                         /note="assembly_name:Contig39"
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|mol_type="genomic DNA"
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                                                                                                              note="assembly_name:Contig38"
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                                            note="assembly_name:Contig40
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169783: contig of 10682 bp in length
169883: gap of unknown length
202983: contig of 33100 bp in length
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19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (31-DEC-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Mar 17, 2000 this sequence version replaced gi:6984442.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 18, clone RP11-119P12
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                       Center project name: L5386
Center clone name: L19 p 12
Center clone name: 119 p 12
Center clone name: 119 p 12
Sequencing vector: M13, M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 161318 bases at least Q40
Consensus quality: 181693 bases at least Q30
Consensus quality: 194050 bases at least Q20
Insert size: 203818; sum-of-contigs
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Quality coverage: 3.2
                                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
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NOTE: This is a 'working draft' sequence. It currently

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consists of 49 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contig are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="18"
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EX 3 (bases 1 to 21648)

RS Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barren, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarateta, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Darellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mtenga, V., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mtenga, V., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mtenga, V., McCarthy, M., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Shuhisang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Enbek, L., Zimmer, A. and Zody, M.
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Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 24, 2002 this sequence version replaced gi:20389460. All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (03-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
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Mus musculus clone RP24-310G22,
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Mammalia; Eutheria; Rodentia;
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                                                                      118162
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* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

1 17004: contig of 17004 bp in length

* 17005 17104: gap of 100 bp

* 17105 19927: contig of 2823 bp in length

* 19928 20027: gap of 100 bp

* 20028 82996: contig of 62669 bp in length

* 20028 82996: contig of 67701 bp in length

* 82797 15567: contig of 67771 bp in length

* 82797 15567: gap of 100 bp

* 150668 216488: contig of 65821 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                 AAATTTTTGATGGCCTTAA 54
                                                                      AAATTTTTGATGGCCTTAA 118180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert size: 198000; agarose-fp
Insert size: 216088; sum-of-contigs
Quality coverage: 11.0 in Q20 bases; agarose-fp
Quality coverage: 10.1 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 214942 bases at least Q40 Consensus quality: 215495 bases at least Q30 Consensus quality: 215807 bases at least Q20
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Center: Whitehead Institute/ MIT Center for Genome
Center code: WIBR
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Center clone name: 310_G_22
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                                                                                                                                                                 Conservative
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82797. .150567
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17105. .. 19927
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/clone="RP24-310G22"
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...17004
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Direct Submission
Submitted (19-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTG; HTGS_PHASE1; HTGS_DRAFT; Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                                         Submitted (29-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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LOCUS
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AC127208.3 GI:30522796
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:22856157.
On Nov 19, 2002 this sequence version replaced gi:22856157.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                             Similarity
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NOTE: This is a "working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                              TTTATAAAGCACTCAATTT 77599
                                                                                                                                                                                                                                                     TTTATAAAGCACTCAATTT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be preserved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: GXOG
Center clone name: GXOG
Center clone name: GXOG
1------ Summary Statistics
Assembly program: Phrap; version 0.990329
Assembly program: Phrap; version 1.990329
Consensus quality: 212567 bases at least Q40
Consensus quality: 214333 bases at least Q20
Consensus quality: 215448 bases at least Q20
Estimated insert size: 217382; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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1662. .2989
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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Pred. No.
228638 bp
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WORKING DRAFT SEQUENCE, 2

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AUTHORS
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Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:23264335.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (14-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Direct Submission
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Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benz
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
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                                                                                Local
          27
                                                      l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  table
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.)
TCTACTCAGAAATTTTTGA 45
                                                                                                                                                                                      66681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: GGJU

Center clone name: CH220-160K20

Center clone name: CH220-160K20

Center clone name: CH220-160K20

Consembly program: Atlas 3.0;

Consensus quality: 221580 bases at least Q40

Consensus quality: 223734 bases at least Q30

Consensus quality: 223977 bases at least Q20

Estimated insert size: 229143; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Baylor Conter code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/
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                                                         Conservative
                                                                                                                                                                              /note="wgs_end_extension
clone_end:T7"
a 44547 c 44747 g 69866 t
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                                                                                                                                                                                                                                                         end_sequence:BH349808"
225364. .227242
                                                                                                                                                                                                                                                                                                           /note="clone_boundary
clone_end:T7
site:EcoRI
                                                                                                                                                                                                                                                                                                                                                                                    end_sequence:BH349810"
complement(224081..22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (4854.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone_end:
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clone_end:Sp6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="CH230-160K20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227242: contig of 227242 bp in length 227342: gap of unknown length 228638: contig of 1296 bp in length.
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                                                                              100.0%;
                                                                                                          8.3%;
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                                                         0,
                                                                                Score 19;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contigs will be indicated in the feature
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                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .5756)
                                                                                                                                                                                                                                                                                                                                                                                    .224845)
                                                                                                          2:
                                                                                                                                                                                      2797 others
                                                                                                          Length 228638;
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                                                           Gaps
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TITLE
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AC023717/c
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                                                                                                   COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Brochto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Jouchah, S., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Jouchah, S., Karly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlsson, E., Kkelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlsson, E., Kkelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Lewis, L.C., Lewis, L., L., Li, J., L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bouck, J. Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carretr, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Davila, M.L., Davis, C., Den, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., M., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., M., Den, A.L., Durbin, K.J., Durbin, M
                                                                                    Submitted (23-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 23, 2002 this sequence version replaced gi:6997287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                     of Molecular and Human
Baylor Plaza, Houston,
3 (bases 1 to 228802)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (17-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 228802)
Worley, K.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                     Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC023717.3 GI:21930215
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Center: Baylor College of Medicine
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                                               23, 2002 this sequence version replaced gi:6997287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unordered pieces.
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                                                    KEYWORDS
SOURCE
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                                                                                                                                             VERSION
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                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                     AC096231
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Query Match
Best Local
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                                                                                                                                                                                                                                                   163358
AC096231 B GI:30522338
AC096231 B GI:30522338
HTG; HTGS_PHASE1; HTGS_DF
Rattus norvegicus (Norway
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                            l Similarity
19; Conserv
                                                                                                 Rattus norvegicus clone CH230-33C23, ***, 2 unordered pieces.
                                                                                                                                             AC096231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.)
NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                   ATTTTCTACCCGGCTCAC 163340
                                                                                                                                                                                                                                                                                    ATTTTCTACCCGGGCTCAC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                64009 a 50361 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assembly program: Phrap; version 0.990329
Consensus quality: 254374 bases at least Q40
Consensus quality: 258311 bases at least Q30
Consensus quality: 271567 bases at least Q20
Estimated insert size: 222216; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: DRJG
Center clone name: RP98-46E23
Center clone name: RT98-46E23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: Plasmid;
Sequencing vector: M13;
Chemistry: Dye-terminator Big Dye: 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site:
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17330
20216
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33624
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9774
12081
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14409
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="RP98-46E23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/(
1. .228802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /chromosome="X"
                                                                                                                                                                                                                                                                                                                      100.0%; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47796: gap of unknown length
95023: contig of 47227 bp in length
95123: gap of unknown length
228802: contig of 133679 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20215: Contig of 2886 bp in length 20315: gap of unknown length 33623: contig of 13308 bp in length 33723: gap of unknown length 47696: contig of 13973 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.hgsc.bcm.tmc.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9673: contig of 9673 bp in length
9773: gap of unknown length
2080: contig of 2307 bp in length
                                                                                                                                                                                                                                                                                                                                                                      8.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Project Information
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                           (Norway
                                                                                                                                                                                                                                                                                                                                                                                                                            49400 g 64230 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap of contig
                                                                                                                                                                                                                                                                                                                          Score 19; DB; Pred. No. 23; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gap of unknown length contig of 2821 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of unknown len
contig of 2128 bp
gap of unknown len
                                         _DRAFT; HTGS_ENRICHED
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                                                                                                                                                                                                                                                                                                                                                 DB
23;
                                                                                                                  DNA **** SEQUENCING
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                                                                                                                                                                                                                                                                                                                                                                    Length 228802;
                                                                                                                                                                                                                                                                                                                                                                                                                                802 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _draft_data.html).
                                                                                                                            IN PROGRESS
                                                                                                                                             HTG 10-MAY-2003
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                                                                                                                                                                                                                                                                                                                              Gaps
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REFERENCE

AUTHORS

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Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Carder, A., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chen, S., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Cleveland, C., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Davila, M. L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Daval, B., Eaves, K., Draper, H., Dugan-Rocha, S., Dunchin, K., Duval, B., Eaves, K., Egan, A., Bsoctto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Garner, T., Garza, M., Gebregocrgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gebregocrgis, E., Geer, K., Gill, R., Gardy, M., Guerra, M., Guevara, W., Gunaratne, P., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladdun, S.L., Hodgson, A., Hogues, M., Hernandez, R., Hines, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Hogues, M., Karpathy, S., Kelly, S., Kelly, S., Kally, S., Kally, S., Kana, Z., King, L., Kovar, C., Kovar, C., Kelly, S., Kelly, S., Kana, Z., King, L., Kovar, C., Liu, J., Liu, J., Loudon, P., Longacre, S., Lopez, J., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Martin, R., Martinez, E., Man, J., Martinez, E., Man, J., Mennen, E., Man, J., Moore, S., Man, J., Martiney, S., Man, J., Mennen, E., Man, J., Martinez, E., Pul, S., Man, S., Martin, R., Martinez, E., Pul, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Popovic, D., Primus, E., Pul, L.-L., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pul, L.-L., Poindexter, A., Popovic, D., Primus, E., Pul, L.-L., Plopper, L., Parks, K., Pasternak, S., Parks, K., Pasternak, S., Panks, K., Paster
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Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Bens Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardense, V., Cardense, V., Cardense, V., Cardense, V., Cardense, M., Cardense, V., Cardense
                                                                                                                                                                                                                                                                             Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:25013165.
The sequence in this assembly is a combination of BAC based reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig descrii in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Worley, K.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat Genome Sequencing Consortium.
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                                   Adams, C., Alder, J.,
                                                                                                                                                              described
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AC095567/c
                                                                                                                                                                                                                             REFERENCE
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ORIGIN
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                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
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REFERENCE AUTHORS TITLE

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Best Local Similarity
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Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, (Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Bad
                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                     Rattus norvegicus (Norway Rattus norvegicus
                                                                                                                                                                                                                                              HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                              AC095567.6 GI:30467314
                                                                                                                                                                                                                                                                                                                                                                                                    AC095567 229140 bp DNA Rattus norvegicus clone CH230-7016, ***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              shotgun sequence only contigs will be indicated in the feature
                                                                                                                        Rattus
                                                                                                                                                        Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.)
NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACTCAGAAATTTTTGATG 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="wgg_contig"
64800 a 42460 c 40825 g 70150 t
                                                                                                                                                                                                                                                                                                                                                                          unordered
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                                                                                         (bases 1 to 229140)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: GERW
Center clone name: CH210-33C23
Center clone name: CH220-33C23
Center clone name: CH220-33C23
Center Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 212493 bases at least Q40.
Consensus quality: 215756 bases at least Q30
Consensus quality: 217525 bases at least Q20
Consensus quality: 217252 bases at least Q20
Estimated insert size: 229406; sum-of-contigs estimation
Quality coverage: 6x in.Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 225592: contig of 225592 bp in length 225692: gap of unknown length 3 229077: contig of 3385 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="CH230-33C23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 19;
Pred. No.
                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
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                                                               Adams, C., Alder, J.
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Benahmed, F.,

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Cardenas, V., Chavez, B., Chen, G., Coyle, M., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, E., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D. Souza, L., Davis, C., Davis, C., Chen, Z., Chu, J., Chen, Z., Chen, Z., Chu, J., Chen, Z., Chu, J., Chen, Z., Chen,
                                                                                                                           Submitted (09-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 9, 2003 this sequence version replaced gi:24940786.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence by sized gaps filled with Ns to the estimated there may be sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (Dases 1 to 229140)
contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,N
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
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                                                                                Rattus norvegicus clone CH230-318P21,
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* Consists of 7 contigs. The true order of the pieces

* tont known and their order in this sequence record is
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218089: gap of unknown length
219464: contig of 1375 bp in length
219564: gap of unknown length
221481: contig of 1917 bp in length
221581: gap of unknown length
221684: gap of unknown length
222644: gap of unknown length
222644: gap of unknown length
224313: contig of 1349 bp in length
224313: dontig of 1349 bp in length
224313: pap of unknown length
224313: pap of unknown length
224314: gap of unknown length
226184: contig of 1771 bp in length
226184: gap of unknown length
226140: contig of 2856 bp in length.
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100.0%; Pred. No.
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On Nov 19, 2002 this sequence version replaced gi:23194968. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Worley,K.C.
Direct Submission
Submitted (05-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 233163)
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                                                                                                                                                                                                                                                        Submitted (19-NOV-2002) Human Genome Sequencing Center, Depa of Molecular and Human Genetics, Baylor College of Medicine,
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                                                                                                                                                                                               of Molecular and Human Genetics, Baylor Baylor Plaza, Houston, TX 77030, USA
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AC099082 Rattus norvegicus

clone

235182 bp ne CH230-11L9,

DNA linear WORKING DRAFT

SEQUENCE

HTG 10-MAY-2003

AC099082.5 GI:30522836 HTG; HTGS_PHASE1; HTGS_ Rattus norvegicus (Norw

HTGS_DRAFT; HTGS_FULLTOP. (Norway rat)

unordered pieces. AC099082

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misc_feature
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                   TTATAAAGCACTCAATTTC 28
                                                                                                                                                                                                                                               end_sequence:BZ141951"
66448 a 39633 c 40161 g 66269 t
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------ Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 209814 bases at least Q40
Consensus quality: 211069 bases at least Q20
Consensus quality: 211069 bases at least Q20
Consensus quality: 211999 bases at least Q20
Estimated insert size: 220261; sum-of-contigs estimation
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/note="clone_boundary
clone_end:T7
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                                                                                                                                      Score 19;
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Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 10, 2003 this sequence version replaced gi:23096197. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas
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Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Ben
Beldwin, D., Balar, J., Blankenburg, K., Blyth, P., Brown, M.,
Briswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (09-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 235182)
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Rattus norvegicus clone CH230-31B17, ***, 9 unordered pieces. AC12629B
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NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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39463 c 41351 g 63457 t
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/mol_type="genomic DNA"
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225906: contig of 1130 bp in length
226006: gap of unknown length
227139: contig of 1133 bp in length
227239: gap of unknown length
227239: gap of unknown length
228691: contig of 1452 bp in length
238791: gap of unknown length
231913: contig of 3122 bp in length
232013: gap of unknown length
231913: contig of 3169 bp in length
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of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Sep 19, 2002 this sequence version replaced gi:21702798.
The sequence in this assembly is a combination of BAC based reads
                                                                                            Direct Submission
Direct Submission
Submitted (22-SEP-2002) Human Genome Sequencing
Submitted (22-SEP-2002) Human Genetics, Baylor College
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                                                                                                                                                                                                                          Submitted (05-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 235700)
                                                                                                                                                                                             Rat Genome Sequencing Consortium.
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and whole genome shotgun sequening reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assembly program: Phrap; version 0.990329
Acconsensus quality: 161627 bases at least Q40
Consensus quality: 168027 bases at least Q30
Consensus quality: 172221 bases at least Q30
Consensus quality: 172221 bases at least Q30
Consensus quality: 172221 bases at least Q20
Estimated insert size: 192265; sum-of-contigs estimation
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
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230824
233137
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10731
224112
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Center clone name: CH230-31B17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Baylor College of Medicine
                                                                                                                                                                                                                                               /note="wgs_contig"
42447. .43559
                                                                                                                                                                                                                                                                                                                                                                           /mol_type= 5----/db_xref="taxon:10116"
end_sequence:BH319296"
                                                     CLone
                                                                                                   /note="wgs_contig"
121152. .121288
                                                                                                                                                                                              /note="wgs_contig"
56213. .57746
                                                                                                                                                                                                                                                                                            /note="wgs_contig"
30002. .31205
                                                                                                                                                /note="wgs_contig"
103185. .104507
                                                                                                                                                                                                                                                                                                                                                                         /clone="CH230-31B17"
                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Rattus norvegicus"

mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation,
                                                  note="clone_boundary:lone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226384: Contig of 1009 by 226384: Gontig of unknown 1 228083: contig of 1599 by 228083: gap of unknown 1 229228: contig of 1045 by 229328: gap of unknown 1 230723: contig of 1395 by 230823: gap of unknown 1 230336: gap of unknown 1 2303236: gap of unknown 1 235236: gap of unknown 1 235700: contig of 2464 by 235700: contig of 2464 by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224111: contig of 213381 bp in length 224211: gap of unknown length 225275: contig of 1064 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10730:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown length
of 1009 bp in length
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unknown length
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220901. .22250, /note="wgs_end_extension clone_end:T7"

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REFERENCE
AUTHORS
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AC108557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muzny, D. Martie, Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anylebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Anylebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chu, J., Chacko, J., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davila, M.L., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Dayal, B., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Paraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Gunarante, P., Haaland, W., Hamilton, C., Hamilton, C., Hamilton, K., Harrandez, J., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Harvey, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Lobow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Mandum, B., Martin, K., Martin, R., Mart
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, R.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
Mawhiney, S., McLeod, M. P., McNeill, T. Z., Meenen, E.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Milosavljevic, A., Morrie, S., Munidasa, M., Murphy, M., Nair, L.,
Morgan, M., Morrie, S., Munidasa, M., Nurphy, M., Nair, L.,
Mankervis, C., Neal, D., Newton, N., Nguyen, N., Norrie, S.,
Nawokelemeh, O., Okwuonu, G., Olarmpunsagoon, A., Pal, S., Parks, K.,
Paternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C.,
Paternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C.,
Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,
Plopper, F., Paul, H., Perez, A., Perez, L., Pfannkoch, C.,
Plopper, F., Paul, H., Perez, A., Perez, L., Pfannkoch, C.,
Reilly, B., Reilly, M., Renty, R., Revees, K., Regler, M.A., Reigh, R.,
Reilly, B., Reilly, M., Renty, R., Rever, K., Rejer, R., Riggs, F.,
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J.,
Sanders, W., Savery, G., Schetzer, S., Scottle, G., Shatsman, S., Shen, H.,
Shetty, J., Shvartebeyn, A., Sisson, I., Sitter, C. D., Smajs, D.,
Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
Taylor, T., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
Wallas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J.,
Wallas, R., Warzen, R., Wei, X., White, F.,
Williams, G., Willson, R., Warzen, R., Wei, X., White, F.,
Wallas, R., Warzen, R., Wei, X., White, F.,
Wright, D., Wang, J., Zhou, X., Zhao, S., Dunn, D., von
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16206 TTATAAAGCACTCAATTTC 16224
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Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Eukaryota; Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus clone CH230-106J14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
23;
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L4, *** SEQUENCING IN PROGRESS
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AUTHORS
TITLE
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JOURNAL
REFERENCE
AUTHORS
TITLE
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238313
241663
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AL Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:23111081.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are oxdered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baylor Plaza, Houston, 3 (bases 1 to 242803)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contige are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: GLEL (enter clone name: CH210-106J14 (enter clone name: CH220-106J14 (enter clone name: CH220-106J14 (enter clone name: KH218-106J14 (enter clone name: KH218-3.0; Assembly program: Atlas 3.0; Consensus quality: 215425 bases at least Q40 (ensensus quality: 21537 bases at least Q40 (ensensus quality: 21637 bases at least Q20 (ensensus quality: 21637 bases at least Q20 (ensensus quality: 21637 bases at least Q20 (ensensus quality coverage: 5x in Q20 bases; sum-of-contigs estimation quality coverage: 5x in Q20 bases; sum-of-contigs estimation
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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clone_end
                                                                                                                                                        /note="wgs_end_extension
clone_end:T7"
                                                                                                                                                                                                                                                                                                     organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                         clone="CH230-106J14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
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    Genome Center

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REFERENCE AUTHORS
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AC097237/c
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Allen, C., Allen, H., Abbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Balswalo, K., Blair, J., Blahkenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chu, J., Clacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, G., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draba, M., Esoetto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garrer, T., Garza, M., Gharrathe, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, A., Hines, S., Hladum, S.L., Hodgson, A., Hogues, M., Hernandez, R., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulseged, H., Lovan, J., Lewis, L., Li, Z., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Manheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Margum, A., Marcin, R., Martinz, E., Montemayor, J., Moore, S., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Mankervis, C., Neal, D., Newton, N., Norris, S., Marken, M., Pal, S., Parks, K., Parsernak, S., Parks, K., Parser, L., Pfannkoch, C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
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clone_end:Sp6"
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235627. .238212
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233686. .235576
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TITLE
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On May 10, 2003 this sequence version replaced gi:22855496.
On May 10, 2003 this sequence version replaced gi:22855496.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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Rat Genome Sequencing Consortium.
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Direct Submission
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Center project name: GGSB

Center clone name: CH230-63H19

Center clone name: CH230-63H19

Center clone name: CH230-63H19

Center Summary Statistics

Assembly program: Atlas 3.0;

Consensus quality: 233600 bases at least Q40

Consensus quality: 236413 bases at least Q20

Consensus quality: 23644 bases at least Q20

Estimated insert size: 244959; sum-of-contigs estimation quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 245082)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                            Project Information
```

COMMENT

JOURNAL

REFERENCE

AUTHORS

```
FEATURES
source
                                                                       * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/cenbank_draft_data.html

* NOTE: This is a 'working draft' sequence. It currently

* consists of I contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

1 245082: contig of 245082 bp in length.
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Location/Qualifiers

_data.html).

Search completed: February 4, 2004, 15:24:52 Job time : 3158 secs

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Minimum
Maximum
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Word size :
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228
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| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981_DAT: *
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981_DAT: *
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984_DAT: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.		Query Match	Query Match Length DB ID	33	ID	Description
1	228	100.0	506	22	AAF30666	Human differential
c 2	20	8.8	205	22	AAF30668	Prostate cancer an
ი ౻	18	7.9	506	22	AAF30666	Human differential
Ω 4	18	7.9	3414	23	AAS83274	DNA encoding novel
ი 5	17	7.5	360	23	ABV36501	Human prostate e
თ	17	7.5	564	24	ABN60692	Human cancer relat
7	17	7.5	580	23	ABL22535	Drosophila melanog
8	17	7.5	601	25	ARX61876	

05-APR-2001.

Human Oestrogen	AAS43104	22	325791	Մ	17	4 5	
Human breast	ABT10147	24	185035	Մ	17	44	
Human cDNA		24	136284	7.5	17	43	O
Genomic D		25	40645	Մ	17	42	
Drosophila melanog	ABL18664	23	30143		17	41	a
cDNA encoding		25	29228		17	40	a
Human musculoskele	AAL3683	22	29228		17	39	G
cDNA encoding	ABX5981	25	28313		17	38	ი
Human musculoskele		22	28313		17	37	ი
Streptococcus pneu	AAV5215	19	28171		17	36	
Human immune/haema		22	23533		17	35	
Human immune/haema		22	23527		17	34	
Human immune/haema	AAK8486	22	23527		17	ω U	
Human novel	AAD16643	22	18657		17	32	
Drosophila		23	7993		17	<u>ω</u>	O
Drosophila		23	6829		17	30	
Human reproductive		22	6352		17	29	
DNA encoding		22	6352	7.5	. 17	28	
Drosophila		23	5790		17	27	
Drosophila	ABL22534	23	2662		17	26	
Human polynucleot		22	2661		17	25	
Human polynucleot		22	2652		17	24	
Human polynucleot		22	2318	7.5	17	23	
Human polynucleoti	AAI60810	22	2309		17	22	
Pain regulated cDN		24	2279	7.5	17	21	
Nucleotide	AAA7573	21	2279		17	20	
Catalase gene	AAX0843	20	2264	•		19	
Streptococcus	ABN6905	24	2070	•		18	
Human zinc	ABV7773	24	1842		17	17	ი
Arabidopsis		21	1675	7.5	17	16	
Human delta-5-desa		24	1357		17	15	
S. pneumoniae		25	1260		17	14	
Streptococcus		19	1252		17	13	
Helicobacter		23	927	7.5	17	12	ი
Human cDNA clone		22	793	٠	17	11	
_		22	773	7.5	17	10	ი
Novel human	ABX61877	25	601		17	9	

ALIGNMENTS

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RESULT 1
AAF30666
exon
                                                                                                                                                                                     11-JUN-2001 (first entry)
                                                                                                                                                                                                     AAF30666;
                                                                                                                                                                                                                    AAF30666 standard; cDNA; 506 BP.
                                                                                                  exon
                                                                                                           Key
                                                                                                                                       human;
                                                                                                                                                                     Human differentially expressed PCA3 cDNA (long form).
                                                                          misc_RNA
                                                                                                                                             PCA3; prostate cancer; antigen; benign prostatic hyperplasia; differential expression; diagnosis; gene therapy; chromosome
                      WO200123550-A2.
                                                                                                                         Homo sapiens
                                                                                                                                        88
                                                                           /number=
27..254
                                     /*tag= c
/number= "
                                                                                                         Location/Qualifiers
                                                           *tag= b
note= "228 bp
                                                   55..506
                                                            insertion"
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ARESULT 2
AAF30668/c
ID AAF306
XX AAF306
XX AAF306
XX DE Prosta
XX PCA3;
KW diagno
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OS Homo s
XX WO2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       additional 228 bp sequence, inserted between exons 3 and 4a. A 2nd camplified fragment (see AAF30667) lacks this additional sequence. The additional sequence interrupts the open reading frame of PCA3 rotein, thereby yielding a truncated PCA3 protein. The shorter form PCA3 RNA is associated with prostate cancer whereas the longer such as benign prostatic hyperplasia. Based on the differential expression of these 2 PCA3 RNA species, protocols for the diagnosis of prostate disease are provided, including a method of diagnosing the presence or predisposition to develop prostate cancer in a patient. Also provided are therapeutic methods that use a nucleic acid encoding a differentially expressed PCA3 mRNA notecule, an antisense sequence, a protein encoded by a differentially expressed PCA3 mRNA, or an antibody raised against such a protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                     PCA3; prostate cancer; antigen; diagnosis; therapy; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acid encoding differentially expressed prostate cancer antigen 3 mRNA containing additional sequence giving rise to long PCA3 mRNA, useful for diagnosis of mammal afflicted with prostate cancer -
                                                                                                                                                                                                                      AAF30668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human prostate cancer antigen additional 228 bp sequence, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3(a); Fig 3; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-258132/26.
                    WO200123550-A2
                                                                                                                                            Prostate cancer antigen 3 (PSA3) nucleic acid.
                                                                                                                                                                                 11-JUN-2001
                                                                                                                                                                                                                                                      AAF30668 standard; cDNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 506 BP; 132 A; 123 C; 108 G; 143 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-SEP-2000; 2000WO-CA01154.
                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                          TACCCGGGCTCACCTCCGTCCCATATTTGTCCTCCACTTTCACAG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTACTCGTTTCTATCCTTCCTACTCACTGTCCTCCCGGAATCCACTACCGATTTTCTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTAAGTGCTTTATAAAGCACTCAATTTCTACTCAGAAATTTTTTGATGGCCTTAAGTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                     TCTTGCCTCGTATTGTCTGACTGGCTCACTTGGATTTATCCTCACGGAGTCTGGATTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTTGCCTCGTATTGTCTGACTGGCTCACTTGGATTTATCCTCACGGAGTCTGGATTTTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTACTCGTTTCTATCCTTCCTACTCACTGTCCTCCCGGAATCCACTACCGATTTTCTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTAAGTGCTTTATAAAGCACTCAATTTCTACTCAGAAATTTTTGATGGCCTTAAGTTCCT
                                                                                                                                                                                                                                                                                                                                                TACCCGGGCTCACCTCCGTCCCTTCCATATTTGTCCTCCACTTTCACAG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence is that of an RT-PCR-amplified fragment ate cancer antigen 3 (PCA3) mRNA that includes an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                        ВP
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Pred. No. 4.8e-108;
                                                                                                          marker; differential expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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RESULT 3
AAF30666/c
ID AAF306
XX AAF306
XX 11-JUN
XX Human
XX PCA3;
KW PCA3;
KW differ
XX Homo s
XX Homo s
XX Homo s
FT exon
FT misc_R
FT exon
FT exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    consecutive nucleotides of the present sequence. Long PCA3 mRNA includes a 228 bp sequence, inserted between exons 3a and 4, which is absent in short PCA3 mRNA. Short PCA3 mRNA is associated with prostate cancer. Long PCA3 RNA is associated with a non-malignant prostatic state. Differential expression of these 2 PCA3 RNA species provides protocols for the diagnosis of prostate disease, including a method of diagnosing the presence or predisposition to develop prostate cancer in a patient. Also provided are therapeutic methods that use a nucleic acid encoding a differentially expressed PCA3 mRNA molecule, an antisense sequence, a protein encoded by a differentially expressed PCA3 mRNA molecule, an antisense mRNA, or an antibody raised against such a protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence comprises nucleotides from human prostate cancer antigen 3 (PCA3) long mRNA (see AAF30666). Claimed isol nucleic acid molecules consist of 10-50 nucleotides which specifically hybridise to a differentially expressed long PCA3 mRNA, and are complementary to, or consist of, at least 10 consecutive nucleotides of the present sequence. Long PCA3 mRN consecutive nucleotides of the present sequence. Long PCA3 mRN consecutive nucleotides of the present sequence.
                                                                               misc_RNA
                                                                                                                                                                                                                                                                                                                            11-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 9 A; 1 C; 8 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acid encoding differentially expressed prostate cancer antigen 3 mRNA containing additional sequence giving rise to long PCA mRNA, useful for diagnosis of mammal afflicted with prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Busse U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-SEP-2000; 2000WO-CA01154.
                                                                                                                                                                                                                                                                                         Human differentially expressed PCA3 cDNA (long form)
                                                                                                                                                                                                                                                                                                                                                                                              AAF30666 standard; cDNA; 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 6; Page 57; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-SEP-1999;
                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                          differential expression; diagnosis; gene therapy; chromosome
human; ss.
                                                                                                                                                                                                                                                          PCA3; prostate cancer; antigen; benign prostatic hyperplasia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                    /number=
27..254
                             /*tag= b
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255..506
                                                                                                                                                       Location/Qualifiers
                                                                                                                       *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claimed isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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'number= "4a"

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RESULT 4
AAS832774/c
ID AAS832
XX AAS832
XX AAS832
XX DNA en
XX DNA en
XX Human;
KW food s
XX Homo s
XX HO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chuman prostate cancer antigen 3 (PCA3) mRNA that includes an additional 228 bp sequence, inserted between exons 3 and 4a. A 2nd camplified fragment (see AAF30667) lacks this additional sequence. The additional sequence interrupts the open reading frame of PCA3 (protein, thereby yielding a truncated PCA3 protein. The shorter form PCA3 RNA is associated with prostate cancer whereas the longer form PCA3 RNA is associated with a non-malignant prostatic state, such as benign prostatic hyperplasia. Based on the differential expression of these 2 PCA3 RNA species, protocols for the diagnosis of prostate disease are provided, including a method of diagnosing the presence or predisposition to develop prostate cancer in a condition. Also provided are therapeutic methods that use a nucleic acid encoding a differentially expressed PCA3 mRNA molecule, an antisense sequence, a protein encoded by a differentially expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acid encoding differentially expressed prostate cancer antigen 3 mRNA containing additional sequence giving rise to long PCA3 mRNA, useful for diagnosis of mammal afflicted with prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                       Human; chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding novel human diagnostic protein #19078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3(a); Fig 3; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-258132/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Busse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-SEP-2000; 2000WO-CA01154
                               31-MAR-2000;
23-AUG-2000;
                                                                                                                     30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                        WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS83274 standard; cDNA; 3414 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of an RT-PCR-amplified fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200123550-A2
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                                                                                                                                                                                                                                                                                                                                                        n; chromosome mapping; gene mapping; gene therapy; forensic;
supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIAGNOCURE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTGCTTTATAAAGCACT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          506 BP; 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTGCTTTATAAAGCACT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chypre C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or an antibody raised against such a protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                               2000US-0540217.
2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0156594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fradet Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22; Length 506; 21;
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RESULT 5
ABV36501/c
ID ABV36501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical a food supplement protein expression or biological activity. It amounts in the polypeptide and polypucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations of another types of data and products dependent on DNA and cressions acid sequences. AAS64197-AAS94564 represent novel human and appearing acquences of the invention.

Note: The sequence data for this patent did not appear in the printed appecification, but was obtained not sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3414 BP; 915 A; 806 C; 940 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chrome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                         Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                        16-SEP-2002
                                                                                                                                                                                                                                                                                                                       ABV36501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID No 19078; 103pp; English.
                                         17-FEB-2000;
16-MAR-2000;
                                                                                                                                                                                                                                                         Human prostate expression marker cDNA 36492.
           25-MAY-2000;
09-JUN-2000;
                                                                                                                    23-AUG-2001.
                                                                                                                                                 WO200160860-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                      20-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATAAAGCACTCAATTTCT 29
                                                                                                                                                                                                                                                                                                                                                  standard; cDNA; 360
                                                                                                                                                                                                                                                                                                                                                                                                                                ATAAAGCACTCAATTTCT 1964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C,
                                         2000US-183319P.
2000US-189862P.
                                                                                      2001WO-US05171
           2000US-207454P.
2000US-211314P.
                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        753 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome
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13-DEC-2000;

2000US-255281P

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RRSULT 6
ABN60808
ID ABN6
XX ABN60
XX ABN6
XX ABN6
XX Huma
XX Huma
XX Huma
XX Homc
XX 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compount of determining whether prostate cancer has metastasized in a patient passessing the aggressiveness or indolence of prostate cancer in
                                                                                                            Escobedo
Lamson G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cytostatic; gene expression;
gene therapy; cancer; tumour; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an a nucleotide sequence given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 360
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                                                         WPI; 2002-241905/29
                                                                                                                                                                                            (CHIR )
(HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                        21-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABN60692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABN60692
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                                                                                                                                                                                                                                                                            16-AUG-2000; 2000US-226326P
                                                                                                                                                                                                                                                                                                                                  16-AUG-2001; 2001WO-US25840
                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200214500-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MILLENNIUM PREDICTIVE MEDICINE
                                                                                                                                                                                            CHIRON CORP. HYSEQ INC.
                                                                                                            J, Garcia
, Scott EM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGATTTTCTATTTCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGATTTTCTATTTCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     related polynucleotide SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP; 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                         PD, Sudduth-Klinger J, Reinhard C,
, Zhang G, Kassam A, Pot D, Labat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; 75 C; 77 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monahan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 isolated nucleic acid molecule (I) comprising in Tables 1-9 (ABV00010-ABV62213) of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 17;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВÞ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene mapping; tissue profiling;
ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for inhibiting prostate cancer
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                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA discloses genomic DNA sequences (ABL16176-ABL30511),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated polynucleotide (ABN27253-ABN33262) with cytostatic activity. The polynucleotide is used to produce a polypeptide, to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and to inhibit tumour growth. The polynucleotide is used as a probe in mapping and tissue profiling. The encoded polypeptide and antibodies to the polypeptide can also be used for therapeutic and diagnostic purposes. The polynucleotide is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster genomic polynucleotide SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expressed genes correlated with a cancerous state of a mammalian and inhibiting tumor growth \boldsymbol{\cdot}
                                                                                                                                                                         genes from Drosophila
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             sequences (ABL01840-ABL16175)
(ABBS7737-ABB72072).
                                                                                                                                  Claim 1; SEQ ID NO 19078; 21pp + Sequence Listing; English
                                                                                                                                                                                     New isolated nucleic acid
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11-JUL-2000;
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                                                                                                                                                                                                                                         PWD,
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        It ransporter subfamily. (I) and the nucleic acid (GABA) neurotransmitter

Ctransporter subfamily. (I) and the nucleic acid encoding it (II) can be

cused as models for the development of human therapeutic targets, aid in

Ct the identification of therapeutic proteins and serve as targets for the

control of the man therapeutic agents that modulate transporter

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control of the protein in biological fluids, and as markers for tissues

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                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 76; 114pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAR-2001; 2001US-0818656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                 invention describes an isolated human
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) KETCHUM K A.
) DI FRANCESCO
) BEASLEY E M.
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                  The invention describes an isolated human transporter peptide (I) that is related to the gamma-aminobutyric acid (GABA) neurotransmitter transporter subfamily. (I) and the nucleic acid encoding it (II) can be used as models for the development of human therapeutic targets, aid in the identification of therapeutic proteins and serve as targets for the development of human therapeutic agents that modulate transporter activity. (I) is used to raise antibodies or to elicit another immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, and as markers for tissues in which the corresponding protein is preferentially expressed. The transporter proteins isolated from humans and their human/mammalian orthologues serve as targets for identifying agents for use in mammalian therapeutic applications, and biological assays related to transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          function. (II) is useful for constructing recombinant vectors, host and transgenic animals; for designing ribozymes; in drug screening; in diagnostic assays for qualitative changes in gene expression, particularly in qualitative changes that lead to pathology; in gene therapy; and to detect mutations in genes encoding transporters. This sequence represents a polynucleotide related to the novel human aminobutyric acid (GABA) transporter related protein of the inventic
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transgenic animal; ribozyme design; drug screening; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pharmacogenomic analysis, for tissue typing and for inhibiting protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human therapeutic targets and serves as target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KETC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-MAR-2001; 2001US-0818656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GONG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gamma-aminobutyric acid; GABA; neurotransmitter transporter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KETCHUM K A.
DI FRANCESCO
BEASLEY E M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GONG F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTCTATTTCTTGCCTC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ketchum
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 76-77; 114pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Francesco V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    뫄
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Pred. No.
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      of the GABA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beasley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s model for developing for human therapeutics
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                                                             use in mammalian
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DT 13-NOV
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transporter subfamily. The proteins and peptides also provide a target for diagnosing a disease or predisposition to disease mediated by the peptide, and are useful for treating a disorder characterised by absence of, inappropriate, unwanted or altered expression of the protein. The antibodies are also useful for assessing normal and aberrant subcellular localisation of cells in various tissues in an organism, in pharmacogenomic analysis, for tissue typing and for inhibiting protein function. (II) is useful for constructing recombinant vectors, host cells and transgenic animals; for designing ribozymes; in drug screening; in diagnostic assays for qualitative changes in gene expression, particularly in qualitative changes that lead to pathology; in gene therapy; and to detect mutations in genes encoding transporters. This sequence represents a polymuclaotide related to the novel human aminobutyric acid (GABA) transporter related protein of the invention.
                                                              The invention relates to novel genes (AAI93926-AAI97963) expressed in human neuroblastoma. The nucleic acids are applicable as a probe or primer in diagnosing the prognosis of human neuroblastoma, malignancy susceptibility indicators or tumour markers for anti-cancer agents. The gene information for diagnosing prognosis is related to factors similar
                                                                                                                                                                                                                                                                    Nucleic acids originating in gene expressed in human neuroblastoma, useful as probe or primer in diagnosing prognosis of human neuroblastoma, malignancy and susceptibility indicator or tumour marker neuroblastoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAR-2001; 2001WO-JP01629.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human neuroblastoma expressed polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 601
                                                                                                                                                                                                                                                                                                                                                                                                             Nakagawara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAI94586 standard; cDNA; 773 BP
                                                                                                                                                                                                     Claim 1; Page 525; 2979pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHIB-)
                                                                                                                                                                                                                                                    anti-cancer agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         HISAMITSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHIBA PREFECTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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100.0%;
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BB
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Query Match Best Local Similarity

7.5%; 100.0%;

Score 17; Pred. No.

68 BD 22;

Query Match

Sequence

793

232

A; 119

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Score 17; 157

Sequence

250 A; 150 C; 120 G; 224 T; 29 other;

for N-myc 773

TrkA

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27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                          sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length CDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
                                                                                                                                                                                                                                                   The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cDNA clone (5'-primer)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH04021
                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-FEB-2001.
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                                              AAB95893 represent human amino
represent oligonucleotides, ali
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNAs -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA;
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                                                 acid sequences; and AAH13629
l of which are used in the exe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      ROM; English.
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                                                   529 to AAH13632
exemplification
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AAS53792/c
ID AAS53792 standard; DNA; 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        片
                   The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are CC genes themselves and the encoded proteins. The prokaryotes used are CC invention is also useful for the identification of potential new targets CC invention is also useful for the identification of potential new targets CC for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, CC and to obtain antibodies capable of binding to the expressed proteins. CC The proteins can be used to screen compounds in rational drug discovery CC programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in CC a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. CC Note: The sequence data for this patent did not form part CC format directly from WIPO at CC fromat directly from WIPO at CC fromat directly from WIPO at
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23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
                                                                                                                                                                                                                                                                                                                                          New polynucleotides for the identification antibiotics, comprise sequences of antisens
Sequence
                                                                                                                                                                                                                                                                                                               Claim 27; Seq ID No 7429; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2001; 2001WO-US09180.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ds; prokaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; 2000US-191078P.
2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-25362SP.
2000US-257931P.
2001US-269308P.
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 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Ohlsen
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHARM
314 A; 176 C; 196 G; 241 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA for cellular proliferation protein
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                                                                                                                                                                                                                                                                                                                                             of antisense
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Query Match

7.5%;

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RESULT 13
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                                                             s. pneumoniae. Its encoded protein, or agonists of it, may be useful as an antibacterial for treatment or prevention of infection, specifically caused by S. pneumoniae (particularly meningitis) but possibly also Helicobacter (pylori (ulcers and gastric cancer). It may be of particular use before insertion of an in-dwelling device or any other invasive procedure. The protein, or nucleic acid encoding it, can also be used in vaccines to induce a cellular and/or humoral immune response, or to screen for other antibacterials. The DNA may also contain flanking sequences that are potential sources of control elements for bacterial can be used diagnostically, e.g. to detect a mutation for servetyping or classifying infectious agents.
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         Query Match
Best Local
                                                                                                                                                                                                                                                                                           e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coding
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                                            Sequence
                                                                                                                                                                                                                                                                                                        New isolated nucleic
                                                                                                                                                                                                                                                                                                                              P-PSDB; AAW61010
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-OCT-1997;
                                                                                                                                                                                                                                  The sequence is that of a coding region isolated from
                                                                                                                                                                                                                                                          Claim 1; Page 104-105; 130pp; English
                                                                                                                                                                                                                                                                                                                                           WPI; 1998-286586/25
                                                                                                                                                                                                                                                                                                                                                                            Black MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9819689-A1
                                                                                                                                                                                                                                                                                                                                                                                                   (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
Local Similarity hes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                 RH,
                                                                                                                                                                                                                                                                                           for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110
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                                            1252
                                                                                                                                                                                                                                                                                                                                                                  Hodgson JE,
Zarfos PN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prevention; meningitis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pneumoniae coding region.
                                            BP; 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORF; open reading frame; antibacterial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= putative gamma-glutamyl phosphate reductase
         100.0%;
                                                                                                                                                                                                                                                                                           acids from Streptococcus pneumoniae anti-bacterial(s) for treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                            A; 235
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         Score 17;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                             pJC,
                                            331 G;
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         DB 19;
                                             335
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                    Length 1252;
                                            other;
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                                                                                                                                                                                                                                                                                            prevention
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DX XX ABNO

       CC identity to any of the 2469 amino acid sequences, identified in the CC specification (available on a computer readable format), or its fragment, CC expressed from 2469 of 2489 identified DNA coding regions from the CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as CC ABS56454. Also included are an antibody which binds one of the CC proteins, treating a patient by administering the protein. DNA or CC antibody (in a composition), a kit comprising first and second primers CC which are the nucleic acid cited above or fragments between nucleotides CC 8-100 of a sequence not defined in the specification, for amplifying a CC where the first primer is substantially complementary to the target sequence not defined in the specification, for amplifying a CC complement of the target sequence, and where the parts of the primers is substantially complementary to the target sequence and the second primer is substantially complementary to the target CC sequence to be amplified, assay comprising contacting a test compound CC with the protein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bacterium, where one or more GC protein and a Streptococcus pneumoniae bacterium, where one or more cCC medicaments for treating or preventing a disease or infection due to streptococcus bacteria, particularly S. pneumoniae, such as pneumoniae, sepsis, otitis media or ear infection. They are also useful in developing vaccines, diagnostics and antibotics. The methods are useful for CC identifying immunodominant proteins. The present sequence is one of the 2489 identified coding region from the genomic sequence. CC format dispected specification, but was obtained in electronic CC format dispected for this patent did not form part
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae type 4 strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-FEB-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-040579/03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       w proteins and nucleic acid molecules from Streptococcus pneumoniae, eful as medicaments for treating or preventing a disease or infectioe to streptococcus bacteria, such as pneumonia, sepsis, otitis media ear infection -
   printed specification, directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INST GENOMIC RES
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CC region used as target for screening drugs useful in treatment of CC diseases involving abnormal lipid metabolism including diabetic neuropathy, arterial hypertension, hypercholesteroolaemia, atherosclerotic heart disease, chronic inflammatory disorders, autoimmune disorders, cC allergic eczema and other atopic disorders, inflammatory process such cas rheumatoid arthritis, diminished lymphocyte proliferation, CC as rheumatoid exthritis, diminished lymphocyte proliferation, CC macrophage-mediated cytotoxicity, monocyte and neutrophil chemotaxis, cc major histocompatibility class II expression and antigen presentation, CC production of pro-inflammatory cytokines (interleukins) and 6, tumour necrosis factor) and adhesion molecule expression, eczema, psoriasis, CC acute respiratory distress syndrome (ARDS), articular cartilage cc degradation (ACD) and cancer. Host cell containing the control cregion of DSD gene is useful for screening for a modulator capable of regulating the expression of a mammalian DSD gene, especially for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               screening compound abnormal lipid metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel control region of delta-5-desaturase gene useful as a target screening compounds useful in the treatment of diseases involving abnormal lipid metabolism including diabetic neuropathy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human delta-5-desaturase (hD5D) gene control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-454647/48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 1; 93pp; English
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jenkins DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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)K, Nwaka SO;
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1976
25-FEB-1999

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16-APR-1999

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21-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

24-MAY-1999

30-APR-1999

30-APR-1999

30-APR-1999

31-MAY-1999

11-MAY-1999

11-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   identifying modulators that modulate lipid metabolism or diabetic neuropathy. The screening method is an assay for identifying modulators that modulate the n-3 lipid metabolic pathway, conversion of 18:3n3-22:6n3, or n-9 lipid metabolic pathway, conversion of 16:0-22:4n9 or n-6 lipid metabolic pathway, conversion of 18:2n6-22:5n6. The human D5D control region provides a powerful tool for dissecting the role of D5D gene expression and inducing modifications, which eliminate or control alterations associated with metabolic disorders. The present sequence is human delta-5-desaturase (hD5D) gene control region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway;
                                                                                                                                                                                                                                                                                                                                                                                       25-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana DNA fragment SEQ ID NO: 70130.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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17; Conserv
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Conservative 0;
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99US-0123548
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99US-0128714
99US-0130077
99US-0130510
99US-0130510
99US-01318510
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0; Mismatches
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01-JUN-1999;
03-JUN-1999;
04-JUN-1999;
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24-MAY-1999;
25-MAY-1999;
27-MAY-1999;
         9908-0136782.
9908-0137528.
9908-0137528.
9908-0137502.
9908-0138040.
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9908-0138040.
9908-0138045.
9908-0139452.
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99US-0146388.
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99US-0149772
99US-0149772
99US-0151066
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99US-0151069
99US-0151066
99US-0159293
99US-0160768
99US-0160768
99US-0160786
99US-0161406
99US-0161360
99US-0161361
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ABV77738/c
ID ABV77738;

XX ABV77738;

XX ABV77738;

XX DE Human zinc finger pr
XX Human; zinc finger pr
XX CN1345803-A.
XX CN1345803-A.
XX CN1345803-A.
XX 26-SEP-2000; 2000CN-
XX Nao Y, Xie Y;
XX Mao Y, Xie Y;
XX Mao Y, Xie Y;
XX Movel polypeptide-hu
PT the polypeptide-hu
PT the polypeptide-hu
PT the polypeptide-hu
PT the present sequence
CC The present sequence
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CC The present seye
CC HIV infection.
    RESULT 18
ABN69051
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Matches 17
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Best Local Similarity
Matches 17; Conserv
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28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                        The present sequence is the coding sequence for human zinc finger protein 10.56. The protein is useful for treating several diseases, such as solid tumours, nervous system disease, haemopathy, development disturbance and HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; zinc finger protein 10.56; tumour; nervous system disease; haemopathy; development disturbance; HIV infection; cytostatic; au gene; ss.
                                                                                                                                                                                                                                                                                                              Novel polypeptide-human the polypeptide -
                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-539319/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-SEP-2000; 2000CN-0125422.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human zinc finger protein 10.56 coding sequence.
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                                                                                                                                                                                                                                                                                 Claim 6; Page 25-26
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                                                                                                                      l Similarity
17; Conserv
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                                                              CATATTTGTCCTCCACT 221
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                                                                                                                        Conservative
                                                                                                                                                                              BP; 516
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99US-0161992.
99US-0161993.
99US-0162142.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "Zinc finger protein 10.56"
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                                                                                                                                     100.0%;
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0; Mismatches
                                                                                                                        Score 17; DB 2; Pred. No. 67; 0; Mismatches
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67;
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RESULT 19
AAX08433
ID AAX08
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AC AAX08
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                                                                                                                                                                                                                                                                                                 Streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus/GAS (Streptococcus/GAS) (Streptococcus/GAS) (Streptococcus/GAS) (Streptococcus/GAS) (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and artibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes.

Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to detect Streptococcus in a biological sample. (I) is used to detect acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity ing composition of immunoassays, and distinguishing/identifying
                                                                                                                                                                                                  Query Match
Best Local S
                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; gene; antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
 AAX08433;
                               AAX08433 standard; DNA; 2264 BP
                                                                                                                                                                                                                                                       Sequence 2070 BP; 751 A; 373 C; 381 G;
                                                                                                                                                                                                                                                                                      Streptococcus proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a protein (ABP25413-ABP30895) from group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Page 3763; 4525pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Telford J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABN69051 standard; DNA; 2070
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                                                                                                                                                                                    l Similarity
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INST GENOMI
                                                                                                                                      CTTTATAAAGCACTCAA 24
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                                                                                                                                                                                    Conservative 0;
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                                                                                                                                                                                                                     7.5%;
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                                                                                                                                                                                                   Score 17; Pred. No.
                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                     565 T; 0 other;
                                                                                                                                                                                                   DB 24;
67;
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                                                                                                                                                                                    0,
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                                                                                                                                                                                                        Inhibition of cytokine mediated immunotoxicity of cells can be achieved by blocking free radical production or the accumulation of free radicals in that cell. Treatment of insulin dependent diabetes mellitus (IDDM) can be achieved by by blocking nitric oxide (NO) production in a pancreatic beta cell and by providing a composition comprising an agent that reduces levels of fatty acids in the cells and protects beta-cells of the subject against lipid-mediated cell death. Cells can also be protected against lipid-mediated cell death. Cells can be used for protecting cells against immunotoxicity by introducing into the cell an antioxidising agent. The methods can be used for protecting cells against immunotoxicity mediated by, e. g. 1L-1 beta, IL-1 alpha, gamma IFN, TNF alpha, TNF beta, IL-8, IL-2, IL-6, IL-2, IL-3, IL-5, IL-7, IL-9, IL-14, IL-17, IL-9, IL-14, IL-17, IL-9, IL-14, IL-17, IL-14, IL-17, IL-15, IL-17, IL-15, IL-17, IL
                                                                                   Matches
                                                                                                       Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protection of mammalian cells against immunotoxicity or lipotoxicity - used for treating, e.g. diabetes, obesity, wasting syndromes, osteoporosis, inflammatory diseases, autoimmune diseases or neurodegenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diabetes mellitus; treatment; therapy; nitric oxide; NO; beta cell; fatty acid; lipotoxic; cytotoxic; cytokine; osteoporosis; inflammatory disease; autoimmune disease; neurodegenerative disease;
                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-153448/13.
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30-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 241-242; 253pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Manganese containing superoxide dismutase; MnSOD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BETA-) BETAGENE INC.
(TEXA) UNIV TEXAS SYSTEM.
  2047
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                                                                                 l Similarity
17; Conserv
                                                                                                                                                                      2264 BP; 634 A; 511 C; 509 G; 610 T; 0 other;
  TCTACTCAGAAATTTTT
                                          TCTACTCAGAAATTTTT 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hohmeier H,
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                                                                                   Conservative
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97US-0055092
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71..1654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human kidney cells.
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                                                                                                     7.5%;
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ı, Thigpen A,
2063
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                                                                                                       Score 17;
Pred. No.
                                                                                     Mismatches
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67;
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RESULT

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RESULT 21
ABL88432
ID ABL88
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AC ABL88
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DT 16-MA
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Best Local
                                                                                                                                                                                                                                                                        scavenging reactive oxygen species in a mammal suspected of having optic neurits, to reduce the effects of demyelinating disease in a mammal and prophylactically used to suppress blood brain barrier disruption in a mammal having identified allergic encephalomyelitis. The rAAV composition is useful for reducing symptoms associated with demyelinating diseases such as optic neuritis, multiple sclerosis, allergic encephalomyelitis, where the symptoms associated with these disease include optic disk edema, increase of optic nerve cell count, disruption of blood brain barrier integrity, increased levels of hydrogen peroxide and demyelination of axons. The present sequence is expressed using the rAAV of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adeno-associated virus; catalase; superoxide dismutase; demyelination; optic nerve; reactive oxygen species; optic neuritis; optic disk edema; demyelinating disease; allergic encephalomyelitis; multiple sclerosis; allergic encephalomyelitis; blood brain barrier; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                        virus (rAAV) composition. The rAAV comprises a polynucleotide sequencoding a mammalian catalase or superoxide dismutase polypeptide reduce demyelination in an optic nerve. The rAAV are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encephalomye\bar{\mathbf{l}}itis, comprises viral constructs expressing catalase superoxide dismutase -
 16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of recombinant adeno-associated virus composition for treating demyelinating disorders e.g. multiple sclerosis and allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA75733 standard;
                            ABL88432;
                                                        ABL88432 standard; cDNA; 2279
                                                                                                                                                                                                                                                 Sequence 2279 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-618854/59
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(QIXX/) QI X.
(HAUS/) HAUSWIRTH W W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The specification describes the use of a recombinant adeno-associated
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X,
                                                                                                                                                 TCTACTCAGAAATTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 74-75; 78pp; English.
                                                                                                                                                                                         Conservative
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 (first entry)
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                                                                                                                                                                                                                                                   642 A; 514 C;
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67;
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                                                    peripheral nervous system, neuropathy; central nervous system; CNS; peripheral nervous system; CNS; parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; SNy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptides
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                                                                                                             Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                                        Human polynucleotide SEQ ID NO 4799.
                                                                                                                                                                     22-OCT-2001
                                                                                                                                                                                                                           AA160810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 41; 213pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying pain-regulating and for diagnosis, by measur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurodegenerative
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17; Conserv
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                                                                                                                                                                                                                           standard; cDNA;
                                                                                                                                                                                                                                                                                                                 TCTACTCAGAAATTTTT 43
                                                                                                                                                                                                                                                                                                                                                                                                           2279 BP; 642 A; 514 C;
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                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              compounds, useful for treating chronic ring binding of compounds to specific
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                             512 G;
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                                                                                                                                                                                                                                                                                                                                                                                                           611 T; 0 other;
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67;
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Homo sapiens

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Best Local (
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25-APR-2000;
09-JUL-2000;
        Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotietic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                              utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.

Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human nucleic acids (AAI57798-AAI61369) the encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                    AAI59024 standard;
                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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                                                                                                                  22-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acids and polypeptides, useful as central nervous system injuries -
                                                                                       polynucleotide SEQ ID NO 1227.
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17; Conserv
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Wang Z,
Zhou P,
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; 2000US-0552317.
; 2000US-0598042.
; 2000US-0620312.
; 2000US-0623450.
; 2000US-062191.
; 2000US-0693036.
; 2000US-07273444.
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Wehrman T, X
Goodrich R,
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(u C, Xue AJ,
Drmanac RT;
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67;
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RESULT 24
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19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                      immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang
Wang
Zhao
Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
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                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 1227; 10078pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
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25-APR-2000;
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Wang Z,
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                                                                                                                   standard; cDNA;
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2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
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Wehrman T, X
Goodrich R,
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Xu C, Xue AJ,
R, Drmanac RT;
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27-APR-2000; 2000US-0569875.
20-JUN-2000; 2000US-0598075.
19-JUL-2000; 2000US-0620325.
01-SEP-2000; 2000US-063561.
20-OCT-2000; 2000US-063325.
30-NOV-2000; 2000US-0728422.
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Zhao QA,
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity inhibit activity and may be useful in the diagnosis and/or activity interests.
Human; cytokine; cell proliferation; cell differentiation; gene the vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
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                                                                                                                                   Human polynucleotide
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                                                                                                                                                                                                                                           AAK51573
                                                                                                                                                                                                                                                                                             AAK51573 standard; cDNA; 2661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2652 BP; 707
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Note: Records for SEQ ID NO 2110 (AAK52581),
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                                                                                                                                                                                                                                                                                                                                                                                                                              2414
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DB; AAM79424.
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the sequence listing
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20-JUN-2000; 2000US-0598075.
19-JUL-2000; 2000US-0620325.
10-SEP-2000; 2000US-0634936.
15-SEP-2000; 2000US-0663561.
20-OCT-2000; 2000US-0693325.
30-NOV-2000; 2000US-0728422.
                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activiny inhibin activity and may be useful in the diagnosis and/or restment of career levicamies.
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Zhao QA,
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27-APR-2000; 2000US-0560875
20-JUN-2000; 2000US-0598075
                                                                                                                                                                                                                                                                                                                            Sequence 2661 BP; 713 A; 638 C; 637 G; 673 T; 0 other;
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                                     pharmaceutical;
                                                    Drosophila;
                                                                                                      26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                      treatment of cancer, leukaemia, nervous system disorders, arthritis and
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DB; AAM78440.
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17; Conserv
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, Wang D,
Yang Y,
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                                                                           melanogaster genomic polynucleotide
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Wejhrman T,
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n T, Goodrich R,
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Drosophila melanogaster

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511) expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid
genes from Drosophila and
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11-JUL-2000; 2000US-0614150.
                                                                  23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                  Drosophila melanogaster genomic polynucleotide SEQ ID NO 17650
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                                                                                                                                                                                                                                                                                                         ABL22059 standard; DNA;
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WPI; 2001-656860/75
                      Venter JC,
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                                                                                                                                                                          Drosophila melanogaster
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                      Adams M,
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Pred. No.
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                           02-MAR-2000;
116-MAR-2000;
117-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-UUN-2000;
28-UUN-2000;
30-UUN-2000;
07-UUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              osteopathic; prostate gland; prostatitis; adenocarcinoma; hair loss; prostatosis; malacoplakia; adenocarcinoma; benign prostatic hypertrophy; hyperplasia; carcinoma; prostate neoplastic disorder; stin aging; reproductive system disorder; autoimmune disorder; urinary system; systemic lupus erythematosus; rheumatoid arthritis; cardiovascular; blood-related disorder; hyperproliferative disorder; respiratory; neurological disorder; endocrine disorder; inflammatory disorder; liver disorder; wound healing; food preservative; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30513) and the encoded proteins (ABB57037-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antianaemic; dermatological; immunosuppressive; antiinflammatory;
antiarthritic; antirheumatic; virucide; hepatotropic; nephrotropic;
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017-NOV-2000
117-NOV-2000
117-NOV-20
The invention relates to novel isolated prostate gland related nucleic acids (I) and polypeptides (II). (I) and (II) are useful for diagnosis, prevention, and/or treatment of diseases and/or disorders of the prostate such as acute non-bacterial prostatitis, chronic non-bacterial prostatitis, chronic non-bacterial prostatitis, prostatodystonia, prostatosis, granulomatous prostatitis, malacoplakia, benign prostatic hypertrophy or hyperplasia, and prostate neoplastic disorders, including adenocarcinomas, transitional cell carcinomas, ductal carcinomas, and squamous cell carcinomas. (I), (II) and antibody to (II) are useful for
                                                                                                                                                                                                                                                  Novel isolated prostate glaand treatment of disorders prostatosis, prostatitis, k
                                                                                                                                                                                                Claim
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enign prostatic orders, including arcinomas, and are useful for

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JAN-2001; 2001WO-US01339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; reproductive system related antigen; reproductive system disorder;
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08-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                Drosophila melanogaster expressed polynucleotide SEQ
                                                                                                                                                                                                                                                                                                                                                                   The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be use in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding
                                                 26-MAR-2002
                                                                                ABL14618;
                                                                                                                                                                                                                                                                                                                      Sequence 6352 BP; 1925 A; 1111 C; 1393 G; 1923
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                              Drosophila; deve pharmaceutical;
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23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                            Drosophila melanogaster
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                                                          23-MAR-2001; 2001WO-US09231.
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17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              standard; DNA;
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Matches 17
                                                                                                                                                                                                                                        Human; lipid metabolism protein; nootropic; neuroprotective; cardiant; cerebroprotective; hepatotropic; antidiabetic; ophthalmic; nephrotropic; immune disorder; autoimmune disease; rheumatoid arthritis; glossitis; systemic lupus erythematosus; conjunctivitis; inflammatory disorder; respiratory disorder; asthma; allergy; CNS disorder; Alzheimer's disease; parkinson's disease; atherosclerosis; cardiovascular disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in lucidating cell signalling and cell-cell interactions in higher eukaryotuciatine development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01876-ABL30511), expressed DNA sequences (ABL01876-ABL30511), expressed DNA sequences (ABL0187737-ABB72072).
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                                                                                                                                                                                                       coronary disease; familial hypercholesterolaemia; hyperlipidaemia;
haematopoietic disorder; hypolipidaemia; lipidosis; Gaucher's disease;
haematopoietic disorder; hypolipidaemia; lipidosis; Gaucher's disease;
herapy; antisense therapy;
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5388..8289
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134.4773
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8290..8420
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14-AUG-2000
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16-MAR-2000;
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18-APR-2000;
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8421..9518
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RESULT 33
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18-DEC-2000;
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02-MAR-2000
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atic; gene therapy; vaccine; metastasis; ds.
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2000US-0179065

2000US-0184664

2000US-0184663

2000US-0184663

2000US-019874

2000US-0198123

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amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (I) corrections and polynucleotides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For certain the production of the prevention, diagnosis and CC example, they may be used to treat disorders associated with decreased certain the preciping mutations or deletions in a patient's genome contract the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) concept caids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent. (C diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic consecutions are sequences from the present invention. AAK854942 to AAK85490 and AAM82169 concept sequences are sequences in the exemplification of the present invention.
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17-NOV-2000;
17-NOV-2000;
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                                                                                                                                                                                                                                                                                         Disclosure;
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                         represent sequences used in the exemplification
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AM82170 to AAM91921. (I) have
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                           4950 and AAM82169 present invention
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b; Pred. No. 67;
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Best Local
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01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                 example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK9492 to AAK82450 and AAM82169 represent formers and in the community of the market invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding useful for preventing, metastasis -
Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                            Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39676.
                                                              07-NOV-2001
                                                                                           AAK84864;
                                                                                                                                                                                                                                                                                                                         Sequence 23527 BP; 6788 A; 5333 C; 5424 G; 5982 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen
                                                                                                                        AAK84864 standard;
                                                                                                                                                                                                                                                                                                                                                         represent sequences used
                                                                                                                                                                                                  4475
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                                                                                                                                                                                                l Similarity
17; Conserv
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2000US-0249265

2000US-0249267

2000US-0249297

2000US-0249297

2000US-0249297

2000US-0250391

2000US-0251030

2000US-0251479

2000US-0251479

2000US-0251486

2000US-0251869

2000US-0251869

2000US-0251869

2000US-0251869

2000US-0251869

2000US-0251869

2000US-0251869

2000US-0251869

2000US-0251869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 39677; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                               Conservative
                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENOME
                                                                                                                      DNA;
                                                                                                                                                                                                                                                         100.0%; F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruben
                                                                                                                        23533 BP
                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                               Score 17;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SM.
                                                                                                                                                                                                                                                                            Pred.
                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                         exemplification
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67;
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                                                                                                                                                                                                                                                                                          Length 23527;
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                       the present invention
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                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                               0
   11-JUL-2000
26-JUL-2000
26-JUL-2000
14-AUG-2000
15-AUG-2000
22-AUG-2000
22-AUG-2000
23-AUG-2000
23-AUG-2000
01-SEP-2000
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28-JUN-2000;
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19-MAY-2000;
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                                         2000US-0230437

2000US-0231242

2000US-0231243

2000US-0231244

2000US-0231413

2000US-0231414

2000US-0231414

2000US-0232141

2000US-0232141

2000US-0232141

2000US-0232398

2000US-0232397

2000US-0232397

2000US-0232397

2000US-0232398

2000US-0232397

2000US-0232398

2000US-0232398

2000US-0232398

2000US-02323063

2000US-0233063
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2000US-0189874.
2000US-0190076.
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2000US-0229287.
2000US-0229343.
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2000US-0224518
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2000US-0216647
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2000US-0227182.
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2000US-0225759
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2000US-0225757
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2000US-0225270
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2000US-0220963
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29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
20-CCT-2000
02-CCT-2000
03-NCV-2000
04-NCV-2000
08-NCV-2000
09-NCV-2000
01-NCV-2000
01-NCV-2000
01-NCV-2000
01-NCV-2000
01-DEC-2000
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01-DEC-2000
08-DEC-2000
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26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
                                                                 2000US-0251856.
2000US-0251868.
2000US-0251869.
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2000US-0235484.
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2000US-0244617.
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                                                   2000US-0251989.
RESULT 36
AAV52155
ID AAV52
XX XAV52
AC AAV52
AC AAV52
AC AAV52
XX Strep
XX Strep
XX Strep
XX Compu
XX Strep
XX WO981
XX WO981
XX WO981
XX 31-OC
XX 31-OC
XX AAV52
PA (HUMA
XX BATAS
PI BATAS
PI KUNSC
XX WPI;
XX WPI;
XX WPI;
XX WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and CT treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased cexpression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC polynucleotides may be used to produce the secreted cell to express the CC grotein. (I) proteins and polynucleotides may be used to prevent, CC clancers and cancer metastases of haematopoietic-derived cells. AAK64703 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703 CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169 CC represent sequences used in the exemplification of the present invention.
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I)
                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae; computer readable medium;
                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae genome fragment SEQ ID NO:22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV52155 standard; DNA; 28171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
 Computer-readable medium with recorded Streptococcus pneumoniae
                                WPI; 1998-272225/24
                                                                                                                                                 31-OCT-1996;
                                                                                                                                                                                  30-OCT-1997;
                                                                                                                                                                                                                    07-MAY-1998.
                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                   23-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4474 ArGGCCTTAAGTTCCTC 4490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 ATGGCCTTAAGTTCCTC 61
                                                                 CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 Similarity 100.0%; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23533 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barash SC,
                                                                 Choi GH,
Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 39676; 3071pp + Sequence Listing; English
                                                                                                                                                 96US-0029960
                                                                                                                                                                                  97WO-US19588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6796 A; 5332 C;
                                                                                Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruben SM;
                                                                                                                                                                                                                                                                                                                 S. pneumoniae; genome; diagnosis; assay;
vaccine; pharmaceutical composition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 17; DB;
; Pred. No. 67;
0; Mismatches
                                                                                  'n,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
                                                                                  Dougherty BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5425
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DB 67;

22; 0,

Length 23533;

Indels

0

Gaps

0,

Fannon

Z

G; 5980 T; 0 other;

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RESULT 37
AAL36829/c
ID AAL36829
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Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA, DNA or cDNA produced from an organism, amplifying nuclect acid molecules whose nucleotide sequence is homologous to amplification primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome of commercial importance, or expression modulating fragments of the S. pneumoniae genome of pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines for S. pneumoniae.
31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAVS2134 to AAVS2524) recorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391 (AAVS2134 to AAVS2524) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating the nucleic acid molecules from the members of the
                                                                                                                                                                                                                                 Cytostatic; immunosuppressive; nootropic; neurop; antiallergic; hepatotropic; antidiabetic; antiini vulnerary; anticonvulsant; antibacterial; antifuc cardiant; gene therapy; cancer; immune disorder;
                                                                                                                                                                                                                     antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein;
                                                                                                                                                                                                                                                                                                                         08-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 28171 BP; 8507 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 273-289; 1409pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pneumoniae
                                                                                                          17-JAN-2001; 2001WO-US01338.
                                                                                                                                   02-AUG-2001.
                                                                                                                                                          WO200155367-A1
                                                                                                                                                                                    Homo
                                                                                                                                                                                                           musculoskeletal system; ds.
                                                                                                                                                                                                                                                                                               Human musculoskeletal system related polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                      8669
                                                                                                                                                                                   sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ll Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTTCTACTCAGAAATT 40
                                                                                                                                                                                                                                                                                                                                                                          standard; DNA; 28313 BP
         2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-0186350.
2000US-018974.
2000US-0199076.
2000US-0199123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.5%; 5-1
100.0%; Pro
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; 6440 G;
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67;
                                                                                                                                                                                                                                                                      neuroprotective; antiviral;
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                                                                                                                                                                                                                                                                                                SEQ ID
                                                                                                                                                                                                                                                                                                NO 3194.
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  18-NIG-2000
22-AUG-2000
22-AUG-2000
23-AUG-2000
30-AUG-2000
01-SEP-2000
01-SEP-2000
01-SEP-2000
01-SEP-2000
05-SEP-2000
06-SEP-2000
06-SEP-2000
08-SEP-2000
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14-AUG-2000
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28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
          26-JUL-2000;
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2000US-0233065.
2000US-0234223.
2000US-0234274.
2000US-0234274.
                                 2000US-0236368.
2000US-02363769.
2000US-0236370.
2000US-0236802.
2000US-0237037.
2000US-0237038.
2000US-0237038.
2000US-0237040.
2000US-0237049.
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2000US-0235834.
2000US-0235836.
2000US-0236327.
2000US-0236327.
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2000US-0232397.
2000US-0232398.
2000US-0232399.
2000US-0232400.
2000US-0232401.
2000US-0233403.
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2000US-0229287
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2000US-0226868
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2000US-0225758
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2000US-0225270
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2000US-0225214
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2000US-0224519
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2000US-0232081
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2000US-0230438
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20-OCT 2000

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01-NOV 2000

08-NOV 2000

017-NOV 2000

17-NOV 2000

17-N
                                                                                                                                                                                                                                                                                                 08-DEC-
11-DEC-
05-JAN-
                                                                                                                              Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.
                                                                                                                                                                                                                                                                    HUMAN
                                                                                                                                                                                                                                 Barash
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2000US-0250391
2000US-0251039
2000US-0251988
2000US-0251479
2000US-0251479
2000US-0251856
2000US-0251868
2000US-0251868
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2000US-0251999
2000US-0259678
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2000US-0249207.
2000US-0249208.
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2000US-0249264.
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for preventing, protein or gene

Example

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Sequence

Listing;

English

The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human

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RESULT 38
ABX59817/C
ID 58878/C
ID 58878/C
XX ABX59
XX AB
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   31-JAN-2000;
04-FEB-2000;
28-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                post-operative tissue repair; limb regeneration; neuronal growth; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; AlDS-related complex; chondrocyte growth; bone regeneration; periodontal regeneration; tissue transport; bone graft; skin aging; keratinocyte growth; hair loss; melanocyte growth; cell proliferation; cell growth; organ transplant; cell differentiation; body height; weight, hair colour; eye colour; skin; percentage of adipose tissue; pigmentation; cosmetic surgery; metabolism; biorhythm; caricadic rhythm; depression; tendency for violence; pain; reproductive capability; hat content; appetite; libido; memory; stress; storage capability; fat content; lipid content; protein content; carbohydrate content; vitamin content; cofactor content;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumaroid arthritis and ulcerative colitis, (c) cardiovascular disorders such as myocardial ischaemias; (d) wound haaling; (e) neurological diseases e.g. cerebral anoxia and epilepsy and (f) infectious diseases such as viral, bacterial, fungal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene; ss; musculoskeletal system antigen; cancer; metastasis; re-vascularisation; thrombosis; arteriosclerosis; mineral content; cardiovascular condition; wound; injury; burn; anglogenesis; ulcer; post-operative tissue repair; limb regeneration; neuronal growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABX59817
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from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Note: The sequence da
                                                                                                                                                                                                                                                                                                                                                          17-JAN-2001;
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17; Conserv
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   2000US-179065P.

2000US-186628P.

2000US-214886P.

2000US-216647P.

2000US-217487P.

2000US-217487P.

2000US-217496P.

2000US-218290P.

2000US-22964P.

2000US-22964P.

2000US-224518P.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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67;
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14-AUG-2000;
114-AUG-2000;
22-AUG-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
05-SEP-2000;
21-SEP-2000;
21-SEP-2000;
21-SEP-2000;
22-SEP-2000;
23-SEP-2000;
29-SEP-2000;
29-S
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14-AUG-2000;
14-AUG-2000;
                  and other cardiovascular conditions; treats wounds due to injuries, burns, post-operative tissue repair, and ulcers; stimulates angiogenesis and limb regeneration; stimulates neuronal growth; can treat and prevent neuronal damage occurring in certain disorders or neurodegenerative conditions, such as, Alzheimer's disease, Parkinson's disease, and AIDS-related complex; stimulates chondrocyte growth, thus they can be used to enhance bone and periodontal regeneration and aid in tissue transports or bone grafts; prevents skin aging due to sunburn by stimulating keratinocyte growth; prevents hair loss, since FGF family members activate hair-forming cells and promotes melanocyte growth; stimulates growth and differentiation of hematopoietic cells and bone marrow cells when used in combination with other cytokines; maintains organs before transplantation or for supporting cell culture of primary tissues; induces tissue of mesodernal origin to differentiate in early
                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence encoding musculoskeletal system associated polypeptides useful for detecting disorders, e.g., cancer or cancer metastases, in animals or humans. The nucleic acid: stimulates re-vascularisation of ischaemic tissues associated with conditions such as thrombosis, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acid molecules associated polypeptides, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ROSE/)
(RUBE/)
(BARA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 3194; 321pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention describes an isolated nucleic acid molecule comprising
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BARASH
increases
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2000US-225268P.
2000US-225270P.
2000US-225758P.
2000US-225757P.
2000US-225934P.
2000US-229343P.
2000US-229344P.
2000US-229344P.
2000US-229344P.
2000US-229344P.
2000US-229344P.
2000US-239344P.
2000US-23423P.
2000US-23423P.
2000US-23423P.
2000US-23423P.
2000US-234597P.
2000US-23636P.
2000US-23636P.
2000US-23636P.
2000US-23636P.
2000US-236370P.
2000US-23703P.
2000US-237
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   or
   decreases
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   the differentiation
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or proliferation
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RESULT 39
AALJ36833/c
ID AALJ368
XX AALJ368
AC AALJ368
AC AALJ368
AC AALJ368
AC Cytost
XW Cytost
XW Cytost
XW antial
XW muscul
XX muscul
XX monoo s
XX MO2001
XX MO200
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CC mammalian characteristics, such as, body height, weight, hair colour, eye
CC colour, skin, percentage of adipose tissue, pigmentation, size, and shape
CC (e.g., cosmetic surgery); modulates mammalian metabolism; changes
CC caricadic rhythms, depression, tendency for violence, tolerance for pain,
CC caricadic rhythms, depression, tendency for violence, tolerance for pain,
CC caricadic rhythms, depression, tendency for violence, tolerance for pain,
CC reproductive capabilities, hormonal or endocrine levels, appetite,
CC libido, memory, or stress; increases or decreases storage capabilities,
CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
CC for other nutritional components. This sequence encodes a novel human
CC musculoskeletal system antigen.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from the US patent office at
CC fip:seqdata.uspto.gov/sequence.html?DocID=20020147140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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31 JJN-2000;
04-FEB-2000;
24-FEB-2000;
24-FEB-2000;
16-MAR-2000;
11-MAR-2000;
11-MAR-2000;
11-MAY-2000;
07-JUN-2000;
07-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cardiant; gene therapy;
neurological disease; in
musculoskeletal system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiunicer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JAN-2001;
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17; Conserv
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2000US-0186350
2000US-019974
2000US-0199123
2000US-0199123
2000US-0209467
2000US-0215135
2000US-021647
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2000US-0216480
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2000US-022963
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2000US-0180628.
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The invention relates to novel genes (AAL34669-AAL37666) and proteins CC (ABB03087-ABB04109) associated with the musculoskeletal system useful CC for preventing, treating or ameliorating medical conditions e.g. by CC protein or gene therapy. The genes are isolated from a range of human CC tissues disclosed in the specification. The nucleic acids, proteins, CC antibodies and (ant)agonists are useful in the diagnosis, treatment CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and CC other cancers of the adrenal gland, bone, bone marrow, breast, CC gastrointestinal tract, liver, lung, or urogenital; (b) immune CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, CC (c) cardiovascular disorders such as myocardial ischaemias; (d) wound CC healing, (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and CC parasitic infections.
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17-NOV-2000
17-NOV
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(a) wound depilepsy; l and

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ABX59821/c
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Best Local
14-AUG-2000
14-AUG-2000
14-AUG-2000
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14-AUG-2000
14-AUG-2000
14-AUG-2000
22-AUG-2000
30-AUG-2000
01-SEP-2000
01-SEP-2000
01-SEP-2000
01-SEP-2000
                                                                                                                                                                   26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              post-operative tissue repair; limb regeneration; neuronal growth; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; AlDS-related complex; chondrocyte growth; bone regeneration; periodontal regeneration; tissue transport; bone graft; skin aging; keratinocyte growth; hair loss; melanocyte growth; cell proliferation; cell growth; organ transplant; cell differentiation; body height; weight; hair colour; eye colour; skin; percentage of adipose tissue; weight; hair colour; eye colour; skin; percentage of adipose tissue; pigmentation; cosmetic surgery; metabolism; biorhythm; caricadic rhythm; depression; tendency for violence; pain; reproductive capability; hormone level; endocrine level; appetite; libido; memory; stress; storage capability; fat content; lipid content; protein content;
                                                                                                                                                                                                                                                                     07-JUL-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                 04-FEB-2000;
28-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                              14-JUL-2000;
                                                                                                                                                                                                                                         11-JUL-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carbohydrate content; vitamin content; cofactor content;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding novel human musculoskeletal system antigen #2165
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           2000US-179065P
2000US-11486P
2000US-214886P
2000US-21647P
2000US-217487P
2000US-217487P
2000US-217487P
2000US-217487P
2000US-220964P
2000US-224518P
2000US-224518P
2000US-22568P
2000US-225267P
2000US-225268P
2000US-2252757P
2000US-225757P
2000US-225757P
2000US-225868P
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Pred. No.
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67;
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27-SEP-2000;

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29-CCT-2000;

02-CCT-2000;

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04-CCT-2000;

05-CCT-2000;

06-CCT-2000;

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05-SEP-2000;
08-SEP-2000;
21-SEP-2000;
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08-DEC-2000;
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2000US-236327P.
2000US-236367P.
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2000US-240960P.
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2000US-244617P.
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Isolated nucleic acid molecules encoding musculoskeletal system associated polypeptides, useful for detecting disorders, e.g. c: cancer

CC conditions, such as Alzheimer's disease, Parkinson's disease, and CC conditions, such as Alzheimer's disease, Parkinson's disease, and CC LIDS-related complex; stimulates chondrocyte growth, thus they can be CC used to enhance bone and periodontal regeneration and aid in tissue CC transports or bone grafts; prevents skin aging due to sunburn by CC members activate hair-forming cells and promotes melanocyte growth; CC stimulates growth and differentiation of hematopoietic cells and bone CC organs before transplantation with other cytokines; maintains CC organs before transplantation or for supporting cell culture of primary CC tissues; induces tissue of mesodermal origin to differentiate in early CC embryos; increases or decreases the differentiation or proliferation of CC embryonic stem cells, besides, haematopoietic lineage; modulates CC colour, skin, percentage of adipose tissue, pigmentation, size, and shape CC (e.g., cosmetic surgery); modulates mammalian metabolism; changes CC mammal's metal state or physical state by influencing biorhythms, CC caricadic rhythms, depression, tendency for violence, tolerance for pain, CC reproductive capabilities, hormonal or endocrine levels, appetite, CC libido, memory, or stress; increases or decreases storage capabilities, cofactors CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors CC mineruloskeletal seate mantigen antigen. The invention describes an isolated nucleic acid molecule comprising a sequence encoding musculoskeletal system associated polypeptides useful for detecting disorders, e.g., cancer or cancer metastases, in animals or humans. The nucleic acid: stimulates re-vascularisation of ischaemic tissue associated with conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions; treats wounds due to injuries, burns, post-operative tissue repair, and ulcers, stimulates angiogenesis and limb regeneration; stimulates neuronal growth; can treat and prevent neuronal damage occurring in certain disorders or neurodegenerative conditions. musculoskeletal system antigen.
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly

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ID ABL186
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                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from the US patent office at
ftp.seqdata.uspto.gov/sequence.html?DocID=20020147140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Venter
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11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 29228 BP; 6450 A; 6876 C; 7498 G; 8404 T; 0 other;
                                                                                                                                                                                                     Sequence 30143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster genomic polynucleotide SEQ ID NO 7465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL18664;
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                                                                                                                                                                                                                                                                            The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PEKE ) PE
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11695
                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
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17; Conserv
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                                                                                                    l Similarity
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CTACCGATTTTCTATTT 11679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 7465; 21pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                    Conservative
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                                                                                                                                                                                                     BP; 8018 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene;
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                                                                                                                                                        7.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cel
                                                                                                                                                                                                     6821 C;
                                                                                              score 17; DB; Pred. No. 67; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17;
; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                  6422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EW;
                                                                                                                           DB 23;
67;
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67;
                                                                                                                                                                                                     8882 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25;
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                                                                                                                                                Length 30143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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                                                                                                 Gaps
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RESULT 42
ABX61804
ID ABX611
XX ABX61804
XX ABX611
XX ABX61
XX Genom

                                                                                                    localisation of cells in various tissues in an organism, in pharmacogenomic analysis, for tissue typing and for inhibiting protein function. (II) is useful for constructing recombinant vectors, host cells and transgenic animals; for designing ribozymes; in drug screening; in diagnostic assays for qualitative changes in gene expression, particularly in qualitative changes that lead to pathology; in gene therapy; and to detect mutations in genes encoding transporters. This sequence encodes a novel human aminobutyric acid (GABA) transporter
                                                                                                                                                                                                                                                                                                                                                                                          in which the corresponding protein is preferentially expressed. The transporter proteins isolated from humans and their human/mammalian orthologues serve as targets for identifying agents for use in mammalian therapeutic applications, and biological assays related to transporter proteins that are related to members of the GABA neurotransmitter transporter subfamily. The proteins and peptides also provide a target for diagnosing a disease or predisposition to disease mediated by the peptide, and are useful for treating a disorder characterised by absence of, inappropriate, unwanted or altered expression of the protein. The antibodies are also useful for assessing normal and abscrant subcellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is related to the gamma-aminobutyric acid (GABA) neurotransmitter transporter subfamily. (I) and the nucleic acid encoding it (II) can be used as models for the development of human therapeutic targets, aid in the identification of therapeutic proteins and serve as targets for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       development of human therapeutic agents that modulate transporter activity. (I) is used to raise antibodies or to elicit another immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, and as markers for tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human transporter protein, related to gamma-aminobutyric acid neurotransmitter transporter subfamily useful as model for developing human therapeutic targets and serves as target for human therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-102517/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic DNA encoding novel human GABA transporter related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABX61804 standard; DNA; 40645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Fig 3; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GONG/)
(KETC/)
(DFRA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-MAR-2001; 2001US-0818656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes an isolated human transporter peptide (I) that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GONG F.

KETCHUM K A.

DI FRANCESCO V

BEASLEY E M.
                                                                             protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
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Query Match
Best Local Similarity
Matches 17; Conserv

ilarity 100.0%; Conservative

0

7.5%;

Score 17; Pred. No. Mismatches

DB 67;

25; 0

Length 40645; Indels

0

Gaps

0

Sequence

40645 BP;

9831 A; 9356 C;

9734

G; 11724 T; 0 other;

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TTTCTATTTCTTGCCTC

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RESULT 43
ABK83575/c
ID ABK835
XX I1-APR
XX ABK835
XX WO2002
XX I1-APR
XX WO2002
XX I1-APR
XX II-APR
XX II
                 CC DNA chip analysis as given in the specification, and comparing CC the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA.

CC Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) CC for an agent capable of modulating GCA or an inflammation (especially CC chronic) in a tissue, an allergic response in a subject to a pathogen or sterile inflammatory disease using the CC gene expression profile; (3) detecting (M4) an inflammation (especially CC chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the CC chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression of the gene is indicative of gene(s) from Gs, where CC the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or inflammation with an agent that modulates the expression of gene(s) form Gs in the tissue. M1 is useful for screening GCA; M2 is useful for GCA preferably in an inflammation in a tissue, M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a pathogen or sterile inflammation (especially chronic) in a tissue, an allergic response in a ninflammation in a tissue, M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a pathogen or sterile inflammation (especially chronic) in a tissue, an allergic inflammatory disease (exposure of a subject to a pathogen or sterile inflammatory disease (exposure of a subject to a pathogen or sterile inflammatory disease (exposure of a subject to a pathogen or sterile inflammatory disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adult respiratory distress syndrome; inflammatory bowel d Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beazer-Barclay Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-OCT-2000; 2000US-237189P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK83575 standard; cDNA; 136284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200228999-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to detecting (M1) granulocyte (GC) activation A), by detecting the level of expression of gene(s) (Gs) identif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENE LOGIC INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Weissman SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146; 114pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamaga S,
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patient, which comprise detecting the level of expression in a tissue sample of two or more genes selected from those shown in ABT09867-ABT1112, where a differential expression of the genes indicates breast cancer. The methods are useful in diagnosing, treating, detecting the progression, and in monitoring treatment of breast cancer in patients. The methods are also useful as a screening tool for agents that modulate the onset or progression of breast cancer. The breast cancer genes may be used as diagnostic markers for the prediction or identification of the malignant state of breast tissue, for confirming the type and progression of cancer, and for drug screening and assays. The present sequence is a coding sequence of the invention.

Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocyte Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                               Diagnosing breast cancer in a patient comprises detecting the level of gene expression in cell or tissue samples, where a differential gene
                                                                                                                                                                                                                                                                                                                                WPI; 2002-674803/72.
                                                                                                                                                                                                                                                                                                                                                                  Orr MS,
                                                                                                                                                                                                                                                                                                                                                                                                                               25-JAN-2001; 2001US-263757P
25-APR-2001; 2001US-286090P
23-MAY-2001; 2001US-292517P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; breast specific gene; breast cancer; differential expression; cytostatic; gene therapy; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human
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                                                                                                                                                                                                  The present
                                                                                                                                                                                                                                  Claim 1;
                                                                                                                                                                                                                                                                  expression is indicative of breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JAN-2002; 2002WO-US02176
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                                                                                                                                                                                                                                                                                                                                                                                               (GENE-) GENE LOGIC INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             breast cancer associated coding sequence SEQ ID
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                                                                                                                                                                                                                                  SEQ ID NO 281; 260pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                               Nation M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTACTCAGAAATTTTT
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                                                                                                                                                                                              invention relates to methods of diagnosing breast
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                                                                                                                                                                                                     cancer in
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                                                                                     The invention relates to a novel isolated peptide comprising or CC consisting of an amino acid sequence selected from an amino acid sequence cof a variant oestrogen receptor protein (e.g. ERbeta), or a fragment of CC 10 amino acids), antibodies against them, nucleic acids encoding CC them (including vectors for transforming cells). The gene for human CC ERbeta is located on chromosome 6q.25.1. The variants are encoded CC by single nucleotide polymorphisms (SNP). The variant peptides and CC corteins can be used in assays to determine the biological colored colored for the protein, to raise antibodies, as a reagent in assays CC designed to quantitatively determine levels of the protein in CC disigned to guantitatively compounds that modulate receptor CC activity and to screen compounds for the ability to stimulate or CC inhibit interacts with the receptor protein and a target molecule CC that normally interacts with the receptor protein e.g. oestrogen. CC that normally interacts with the receptor protein, to assess expression in CC disease states e.g. cardiovascular disease and autoimmune disease (e.g. Cartenorous and a transfer in addition in the action to the control of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oestrogen receptor gene and protein polymorphisms useful for diagnosis of individuals at risk of developing bone disorders \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; Oestrogen receptor beta; ERbeta; ds; SNP; chromosome 6q.25.1; single nucleotide polymorphism; cardiovascular disease; autoimmune disease; systemic lupus erythematosus; arthritis; rheumatism; osteoarthritis; osteoporosis; breast cancer; endometrial cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub.published_pct_sequences.
                    osteoporosis, breast cancer and endometrial cancer. In addition the antibodies can be used in pharmacogenomic analysis and inhibiting protein function, e.g. blocking the binding of the oestrogen receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Figure 1; 245pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-FEB-2000; 2000US-0183755.
24-JAN-2001; 2001US-0768185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-FEB-2001; 2001WO-US05360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS43104 standard; DNA; 325791 BP
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to a binding partner such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTAAGTGCTTTATAAAG 62483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cassel MJ,
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                         Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                Sequence 325791 BP; 94098 A; 68292 C; 67970 G; 95431 T; 0 other
                                                                                                        human ERbeta gene.
                                                                                                                       encoding the proteins can be used as probes, primers, chemical intermediates and in biological assays. The present sequence is the
45
 ATGGCCTTAAGTTCCTC 61
                            Conservative
                                       100.0%;
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67;
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Search completed: February 4, 2004, 15:29:44
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Match
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        US-08-961-527-22

US-09-313-294A-6323

US-09-702-705-1614

US-09-702-705-1614

US-09-702-705-46

US-09-702-705-46

US-09-702-705-46

US-09-702-705-46

US-09-702-705-794

US-09-702-705-794

US-09-702-705-794

US-09-702-705-794

US-09-702-705-794

US-09-702-705-188

US-09-205-788-67

US-09-205-788-67

US-09-205-784-508-1

US-09-205-784-508-1

US-09-205-784-508-1

US-09-205-784-508-1

US-09-784-508-1

US-09-784-508-1

US-09-784-508-1

US-09-784-508-1

US-09-784-508-1
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US-09-126-109-9
US-09-620-312D-916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 parameters:
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1437.648 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Compugen Ltd
                                                                                                                                                     Sequence 13, Appl
Sequence 13, Appl
Sequence 46, Appl
Sequence 46, Appl
Sequence 794, App
Sequence 794, Appl
Sequence 67, Appl
Sequence 18, Appl
                                                                                                                                                                                                                                                                 Sequence 916, Appl
Sequence 22, Appl
Sequence 6323, Ap
Sequence 1614, Ap
Sequence 1614, Ap
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                                   Sequence
Sequence
Sequence
                                                                            Sequence
Sequence
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Sequence
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                                                                                                                                                                                                                                                                                                                                                   Sequence 248, App
                        Sequence
                                                                                                     Sequence
                                                                                                                  Sequence
                                                                                                                                  Sequence
                                 254, App
51, Appl
1108, Ap
16, Appl
           3, Appl 2461, A
                                                                          Appli
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6, App
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RESULT 1 US-09-107-532A-248

ALIGNMENTS

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Sequence 248, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                        INFORMATION FOR SEQ ID NO: 248:
SEQUENCE CHARACTERISTICS:
LENGTH: 1896 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-7un-1998
PRIOR APPLICATION NUMBER: 60/085,598
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: 1414
FILING DATE: 1414
FILING DATE: 1414
ANDE: Ariniello, pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-8277
TELEPHONE: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM IS09660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                FEATURE:
                                                                                              ORIGINAL SOURCE:
                                                                                                                 HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Waltham
STATE: Massachusetts
NAME/KEY: misc feature LOCATION: (B) LOCATION 1...1896
                                                                     ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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US-09-126-109-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; SEQUENCE DESCRIPTION: SEQ ID NO: 248: US-09-107-532A-248
                                                                                                           US-09-126-109-9
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                                                Matches
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Patent No. 6:
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                                                                             Query Match
                                                                                                                                                                                  TELEFAX: (512) 474-757
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2264 base pair
                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/
FILING DATE: 30-UUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US UNA
FILING DATE: 03-MAR-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION WHERE: US/09/126,109 FILLING DATE: 30-UUL-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                       TOPOLOGY: 1:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rhodes, Christon
APPLICANT: Hugl, Sigrun R.
APPLICANT: Cousin, Sharon
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: TO NO-N
                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                           NAME: McMillian, Nabeela R. REGISTRATION NUMBER: P-43,3 REFERENCE/DOCKET NUMBER: UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: P.O. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 TTTTCTATTTCTTGCCT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
27 TCTACTCAGAAATTTTT 43
                                                                                                                                                                nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Arnold, Wh
P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                  (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thigpen, Anice
Hohmeier, Hans-Ewald
Newgard, Christopher B.
                                               7.5%;
llarity 100.0%;
Conservative
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Shimabukuro, Michio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                  single
                                                                                                                         DNA (genomic)
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              White & Durkee
                                                                                                                                                                                                                                                                                                                                                     US Unknown
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                                                             Score 17; DB 3; Pred. No. 7.3;
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Pred. No.
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                                                Mismatches
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                                             0; Indels
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                                                                        Length 2264;
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APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 656662el Nucleic Aci
TITLE OF INVENTION: No. 656662el Nucleic Aci
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04.25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOPTWARE: pt FL genes Version 1.0
SEQ ID NO 916
LENGTH: 2318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: (103)..(1686)
US-09-620-312D-916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-620-312D-916
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                                                                                                                                                                                                                                                                 Sequence 22, Apprisequence No. 6420135
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity Matches 17; Conserv
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                                                                                                                                                                                                                                                      Patent No. 6420135
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
                                                                                        STREET: 9410
STREET: PACKVILLE
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                               TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 391
                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                    APPLICANT: Charles Kunsch
TITLE OF INVENTION: Strept
OPERATING SYSTEM:
                                                                                    COUNTRY:
                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                          27 TCTACTCAGAAATTTTT 43
                                                                         20850
                                                                                                                                                                                                                                                                                                                                                                                      TCTACTCAGAAATTTT 2094
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Wang, Dunrui
Wang, Zhiwei
John Tillinghast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Asundi, Vinod
Zhang, Jie
Ren, Feiyan
Chen, Rui-hong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
Xue, Aidong J.
Yang, Yonghong
                                                                                                                                                                                                                                                                                           Application US/08961527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhou,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang, Jian-Rui
                                                                                                                                              9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                               Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chenghua
ldi, Vinod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                    / 100.0%; F1
                                                                                                                                                               Genome Sciences,
MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.5%; Score 17; DB 4;
100.0%; Pred. No. 7.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                    pneumoniae Polynucleotides and Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2318,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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SOFTWARE: ASCII Text CURRENT APPLICATION DATA:

FILING DATE:

APPLICATION NUMBER: US/08/961,527

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RESULT 6
US-09-702-705-1614/c
US-09-702-705-1614, Application US/09702705
; Patent No. 6504010
; Patent No. 6504010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PER
SEQ ID NO 6323
LENGTH: 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE, DOCKET NUMBER: PB34
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6323, Application US/09313294A Patent No. 6476212
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                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT FACATION NUMBER: US/09/313,294A
CURRENT FILLING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTMARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lalgudi, Raghunath V. APPLICANT: Ito, Laura Y. APPLICANT: Sherman, Bradley K.
   APPLICANT:
                                                                                                                                                                                                                                                                                                              NAME/KEY: unsure
LOCATION: 92, 254, 257, 294
OTHER INFORMATION: a, t, c,
                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6476212 700351604H1
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 17; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 28171 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6998 ATTTCTACTCAGAAATT 7014
                                                                                                                                                    144 CTTGCCTCGTATTGTC 129
                                                                                                                                                                                      122 CTTGCCTCGTATTGTC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 ATTTCTACTCAGAAATT 40
Wang, Tongtong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.5%; Score 17; DB 4; Length 28171; ilarity 100.0%; Pred. No. 7.9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                     100.0%; FI
                                                                                                                                                                                                                                          7.0%; Score 16;
100.0%; Pred. No.
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                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                            DB 4; Length 300; 23;
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RESULT 8
US-09-702-705-13
; Sequence 13, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:

APPLICANT: Wang, Tongtong

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APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jame
APPLICANT: Fen, Liqun
APPLICANT: Fen, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1614
LENGTH: 439
TYPE: DNA
ORGANISM: Homo sapiens
US-09-702-705-1614
7.0%; Score 16; DB 4
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                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-736-457-1614
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                                                                                                                                                                     TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 20121.478C15
CURRENT APPLICATION NUMBER: U8/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1614
LENGTH: 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFO
APPLICANT:
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Best Local Similarity
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193
                       212 GTCCTCCACTTTCACA 227
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16; Conserv
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Carter, Darrick
Retter, Marc
Mannion, Jane
GTCCTCCACTTTCACA
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Vedvick, Tom
Carter, Darrick
Retter, Marc
Mannion, Jane
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Wang, Aijun
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Lodes, Michael A.
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Lodes, Michael A.
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Chaitanya

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APPLICANT: MAILLANT: MAILLANT: APPLICANT: FAR, Liqun

ITITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

ITITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.478C14

CURRENT APPLICATION NUMBER: US/09/702,705

CURRENT FILING DATE: 2000-10-30

NUMBER OF SEQ ID NOS: 1833

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 13

LENGTH: 493

TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KBY: misc_feature
LOCATION: (1)...(493)

OTHER INFORMATION: n = A,T,C or G

US-09-702-705-13
                                                                                                                   SOFTWARE: FASTSEQ for Windows V
SEQ ID NO 13
LENGTH: 493
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1) ... (493)
OTHER INFORMATION: n = A,T,C ox
US-09-736-457-13
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US-09-736-457-13
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                                                                        Query Match
Best Local Similarity
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CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
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                             212 GTCCTCCACTTTCACA 227
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   GTCCTCCACTTTCACA 428
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Retter, Marc
Mannion, Jane
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Lodes, Michael J
Fanger, Gary
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Retter, Marc
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APPLICANT: Carter, Darilo,
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
ITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
ITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121 478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 183
SOPTWARE: FASTSEQ FOR WINDOWS Version 3.0
SEQ ID NO 46
LENGTH: 516
TYPE: DNA
ORGANISM: Homo sapien
US-09-702-705-46

TYPE: DNA
ORGANISM: Homo sapien
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APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Renter, Marc
APPLICANT: Fan, Liqun
APPLICANT: Wang, Aijun
APPLICANT: Wang
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US-09-702-705-46
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CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 46
SEQ ID NO 46
                                                                                 Query Match
Best Local Similarity
Matches 16; Conserv
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212 GTCCTCCACTTTCACA 227
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Carter, Darrick
Retter, Marc
Mannion, Jane
Fan, Liqun
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Lodes, Michael A.
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Bangur, Chaitanya
Lodes, Michael A.
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Pred. No.
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Pred. No.
                                                                                       Mismatches
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413 GTCCTCCACTTTCACA 428

US-09-702-705-794/c

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; SOFTWARE: FastSEQ for W:
; SEQ ID NO 794
; LENGTH: 970
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-736-457-794
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; ORGANISM: Homo sapiens
US-09-702-705-794
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US-09-736-457-794/c
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SEQ ID NO 794
LENGTH: 970
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Best Local Similarity
Matches 16; Conservat
                                                    Query Match
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Matches 16; Conserv
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1860-413-13
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CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
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                   212 GTCCTCCACTTTCACA 227
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GICCICCACTITCACA 208
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Vedvick, Tom
Carter, Darrick
Retter, Marc
Mannion, Jane
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Vedvick, Tom
Carter, Darrick
Retter, Marc
Mannion, Jane
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Lodes, Michael A.
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Bangur, Chaitanya
Lodes, Michael A.
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                                                    7.0%; Score 16; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
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r, Chaitanya S.
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                                                         Mismatches
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US-09-205-258-67/c
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GENERAL INFORMATION:
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TITLE OF INVENTION: 207 Human Secreted Proteins
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                                                                                                 FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,374
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,915
FILING DATE: 1997-06-06
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                              APPLICATION NUMBER: 60/048,917
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,949
FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/049,019
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,970
FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,875
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APPLICATION NUMBER: 60/049,373
                                                                                                                                                                                                                        APPLICATION NUMBER: 60/048,916
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/048,892
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/048,901 FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,974 FILING DATE: 1997-06-06
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NUMBER: 60/048,883

DATE: 1997-06-06

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US-09-453-702B-188/c
Sequence 188, Application US/09453702B
Parent No. 6365723
GENERAL INFORMATION:
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NAME/KEY: SITE
LOCATION: (668)
OTHER INFORMATION: n
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EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER APPLICATION NUMBER: 60/092,921
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NUMBER OF SEQ ID NOS: 1227
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EARLIER APPLICATION NUMBER: 60/094,657
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TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: (1113)
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LOCATION: (111)
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OTHER INFORMATION: n
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LOCATION: (1015)
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LOCATION: (745)
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              Welch, Rod
TITLE OF INVENTION: No. 6365723el Sequences
NUMBER OF SEQUENCES: 265
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ER FILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048,898
ER FILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048,962
ER FILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/048,963
ER APPLICATION NUMBER: 60/048,963
                                                                                                                APPLICANT: Blattner, Frederick R.
CORRESPONDENCE ADDRESS
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Plunkett, Gu,
Tah. Rod
                                                                                   Burland, Valerie
Perna, Nicole T.
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TOPOLOGY: linear;

MOLECULE TYPE: DNA (genomic);

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-453-702B-188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6521236
GENERAL INFORMATION:
APPLICANT: Willem
APPLICANT: Sonder
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PRILLICATION: 435
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/211,15(
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                                                                                                                ZIF: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/504,617
                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Vector vaccines of r
TITLE OF INVENTION: Feline herpesviruses
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                  CITY: Rockville
                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Akzo No. 6521236el
STREET: 1330 Piccard Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
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MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
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STRANDEDNESS: double
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STREET: 1 South Pinckney Street
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TELEFAX: (608) 251-9166
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Sondermeijer, Paulus Jacobus Antonius
VENTION: Vector vaccines of recombinant
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                                        08/211,150
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ENFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

ENGTH:

6154 base pairs

TELEPHONE:

(301)

258-5200

NAME: Gormley, Mary E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:

ATTORNEY/AGENT INFORMATION:

OTHER INFORMATION: /label= ORF-1 FEATURE: NAME/KEY: CDS LOCATION: 1460..3058 OTHER INFORMATION: /label= ORF-2

NAME/KEY: CDS LOCATION: 127..1281

LOCATION: 3055..3357
OTHER INFORMATION: /label= ORF-3

NAME/KEY:

CDS

STRAIN: G2620 IMMEDIATE SOURCE:

ORGANISM:

Feline herpesvirus

(FHV-1)

CLONE:

Lambda FHV04

MOLECULE TYPE: 1

STRANDEDNESS:

nucleic acid

COPOLOGY:

linear

DNA (genomic) double

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US-09-177-249-6
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                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09177249
Patent No. 6229064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
         APPLICANT: Harada, John
APPLICANT: Harada, John
APPLICANT: Goldberg, Robert B.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Nucleic Acids That Control Seed and
TITLE OF INVENTION: Development in Plants
FILE REFERENCE: 023070-086120US
CURRENT APPLICATION NUMBER: US/09/177,249
CURRENT FILING DATE: 1998-10-22
EARLIER APPLICATION NUMBER: US/09/071,838
EARLIER FILING DATE: 1998-05-01
                                                                                                                                                                                                APPLICANT: Ohad, Nir
APPLICANT: Kiyosue, Tomohiro
APPLICANT: Yadegari, Ramin
APPLICANT: Margossian, Linda
                                                                                                                                                                                                                                                                                                 ENERAL
                                                                                                                                                                                                                                                                            ENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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LOCATION:
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LOCATION: complement (4256..4897)
OTHER INFORMATION: /label= ORF-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: complement (5138..6142)
OTHER INFORMATION: /label= ORF-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              3256 CTACCGATTTTCTATT 3241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTACCGATTTTCTATT 120
ID NOS:
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3505..3963
3507... /label= ORF-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.0%; Score 16;
100.0%; Pred. No.
tive 0; Mismatcl
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26;
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                                                                                                                               and Fruit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09922445
Patent No. 6528268
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver.
SEQ ID NO 6
LENGTH: 7015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.1 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: GG126US
CURRENT APPLICATION NUMBER: US/09/922,445
CURRENT FILING DATE: 2001-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Andersson, APPLICANT: Berglund,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTION OF HEART FAILURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (3)..(7013)
OTHER INFORMATION: fertilization-independent endosperm 1 (FIE1)
OTHER INFORMATION: SET/polycomb gene genomic sequence reading frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1)..(7014)
OTHER INFORMATION: fertilization-independent endosperm
OTHER INFORMATION: SET/polycomb gene genomic sequence
                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (24801). (24801)
OTHER INFORMATION: nucleotide
OTHER INFORMATION: A or G
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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LOCATION: (3)
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OTHER INFORMATION: fertilization-independent
OTHER INFORMATION: SET/polycomb gene genomic
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LOCATION: (1)
                                                                                                                                                                                            OTHER INFORMATION: nucleotide OTHER INFORMATION: T or C
                                                                                                                                                                                                                                                                                                                                      LOCATION: (1)..(26 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: homo sapiens FEATURE:
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                                                                               COCATION: (26253).
                                                                                                                                        LOCATION: (26157)..(26252)
OTHER INFORMATION:
                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (24941)..(24941)
                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: 5'UTR
                               OCATION: (26402).
OTHER INFORMATION:
                                                                  NAME/KEY: exon
                                                                                                                                                                         NAME/KEY: exon
                NAME/KEY:
                                                                                                                       NAME/KEY: Intron
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nes 16; Conserv
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                                                                                                       (26253)..(26401)
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(26544) .. (27024)
                                                   (26402) . . (26543)
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100.0%; Pred. No.
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                                                                                                                                                                                                            a single nucleotide polymorphism
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sequence reading frame
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US-09-922-445-1
Query Match 7.0%; Score 16; DB 4; Best Local Similarity 100.0%; Pred. No. 28; Matches 16; Conservative 0; Mismatches
                                                                                      NAME/KEY: exon
LOCATION: (3842)..(38653)
OTHER INFORMATION:
OTHER INFORMATION:
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank/AC004923
DATABASE ENTRY DATE: 1999-12-21
RELEVANT RESIDUES: (1)..(38653)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (27645)..(27645)
OTHER INFORMATION: nucleotide 27645 is a single nucleotide polymorphism which can
OTHER INFORMATION: C or G
                                                                                                                                                                                                                          LOCATION: (36524).
OTHER INFORMATION:
                                                                                                                                                                                                                                                                            LOCATION: (36405)..(36523)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feat
LOCATION: (32614).
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: nucleotide 32163 is a single nucleotide polymorphism which can OTHER INFORMATION: A or C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (27645)...(27
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JOCATION: (34589)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AME/KEY: Intron
OCATION: (27179)
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OCATION: (31028)..(31747)
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JOCATION: (308)
                                                                                                                                                                                                                                                                                                                                        THER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            OCATION: (34315)..(34588)
THER INFORMATION:
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OCATION: (32163)..(32
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OCATION: (33598)..(34314)
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                                                                                                                                                                                                                                            ..(38341)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleotide 32614 is a single nucleotide polymorphism which can
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                                    Length 38653;
   Indels
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 Gaps
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SEQ ID NO 1
LENGTH: 319608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cohen,
APPLICANT: Blumen
APPLICANT: Chumak
APPLICANT: Bougue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 09/416,384 PRIOR FILING DATE: 1999-10-12 NUMBER OF SEQ ID NOS: 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/539,333D CURRENT FILING DATE: 2000-03-30 PRIOR APPLICATION NUMBER: US 60/126,903 PRIOR FILING DATE: 1999-03-30 PRIOR APPLICATION NUMBER: US 60/131,971 PRIOR FILING DATE: 1999-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bihain, Bernard
APPLICANT: Essioux, Laurent
TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
FILE REFERENCE: GENSET.047AUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/145,915
PRIOR FILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: US 60/146,453
PRIOR FILING DATE: 1999-07-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1999-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/132,065
PRIOR FILING DATE: 1999-04-30
                                                                                                                                                                                                                             FEATURE: exon
NAME/KEY: exon
COCATION: 18778...18862
COCATION: PARTION: exon
                                                                         NAME/KEY: exon
LOCATION: 29388..29502
OTHER INFORMATION: exon
                                                                                                                                                        LOCATION: 25593..25740 OTHER INFORMATION: exon
                                                                                                                                                                          NAME/KEY: exon
LOCATION: 25593..25740
                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 1108..1289
OTHER INFORMATION: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 31..1107
OTHER INFORMATION: 5'regulatory region g35018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
NAME/KEY: exon
LOCATION: 29967..30282
OTHER INFORMATION: exon E g35018 gene
                                                                                                                                                                                                                                                                                                                                        NAME/KEY: exon
LOCATION: 14877
                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: exon
LOCATION: 1108.
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                                                            FEATURE:
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OTHER INFORMATION: exon
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FILING DATE: 1999-07-29
APPLICATION NUMBER: US 60/162,288
FILING DATE: 1999-10-28
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Bougueleret, Lydie
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NAME/KEY: exon
LOCATION: 231272..231412
OTHER INFORMATION: exon
                                                                                                                                NAME/KEY: exon
LOCATION: 230408..230721
OTHER INFORMATION: exon P
NAME/KEY: exon
LOCATION: 231787..231880
OTHER INFORMATION: exon O2 complement g34872 gene
                                                                                                                                                                                                      NAME/KEY: exon
LOCATION: 229647..229742
OTHER INFORMATION: exon X
                                                                                                                                                                                                                                                                LOCATION: 217027..217061
LOCATION: 217027..exon Q1
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LOCATION: 216661..217061
OTHER INFORMATION: exon
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LOCATION: 94124..94964
OTHER INFORMATION: exon g35017
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LOCATION: 65505..65853
OTHER INFORMATION: exon G
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'AME/KEY: exon
'COCATION: 215819..215975
DTHER INFORMATION: exon Rbis
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OCATION: 216836..216915

OTHER INFORMATION: exon
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LOCATION: 65854..67854
OTHER_INFORMATION: 3'regulatory region g35018 gene
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OCATION: 216661..216952
THER INFORMATION: exon Qbis complement g34872 gene
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OCATION: 213818..2158
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JOCATION: 215702..215746
WITHER INFORMATION: exon U
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OCATION: 215819..215941
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OTHER INFORMATION: exon '
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NAME/KEY: exon
LOCATION: 64666..64812
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DCATION: 201188..201234
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Best Local Similarity
Matches 16; Conserv
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NAME/KEY: exon
LOCATION: 292653..292841
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LOCATION: 241686..243685
OTHER INFORMATION: 5'regulatory region g34872
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LOCATION: 239719..239807
OTHER INFORMATION: exon N2
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OTHER INFORMATION: exon
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LOCATION: 240528..240994
OTHER INFORMATION: exon P
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LOCATION: 240528..240824
OTHER INFORMATION: exon M862 complement
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LOCATION: 240528..240644
OTHER INFORMATION: exon MS2
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LOCATION: 240528..240569
OTHER INFORMATION: exon M1117
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LOCATION: 239719..239853
OTHER INFORMATION: exon
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LOCATION: 231870..231879
OTHER INFORMATION: exon O1
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LOCATION: 290652..292652
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OTHER INFORMATION: exon M1
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LOCATION: 240528..240617
OTHER INFORMATION: exon M1069
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LOCATION: 240528..240596
OTHER INFORMATION: exon M1090 complement g34872 gene
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LOCATION: 237406..237428
OTHER INFORMATION: exon 1
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LOCATION: 234174..234321
OTHER INFORMATION: exon O
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TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENE,
FILE REFERENCE: 53.US15.CIP
CURRENT APPLICATION NUMBER: US/09/679,409
CURRENT FILING DATE: 2000-10-03
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 199122..201122
OTHER INFORMATION: 5'regulatory region
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OTHER INFORMATION: exon S2
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LOCATION: 201123..201234
OTHER INFORMATION: exon S
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LOCATION: 238715..238919
OTHER INFORMATION: exon V3
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OTHER INFORMATION: exon V4
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OTHER INFORMATION: exon T
OTHER INFORMATION: exon
                                                      LOCATION: 244353..244561
OTHER INFORMATION: exon
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LOCATION: 240440..240673
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LOCATION: 216836..216994
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o. 6555316
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                    246273..247802
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Bougueleret, Lydie
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LOCATION: 160876
OTHER INFORMATION: 99-24634-108 :
NAME/KEY: allele
LOCATION: 168974
OTHER INFORMATION: 99-7652-162 :
NAME/KEY: allele
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OTHER INFORMATION: 8-300-221
NAME/KEY: allele
LOCATION: 202679
OTHER INFORMATION: 8-300-193
NAME/KEY: allele
LOCATION: 203378
OTHER INFORMATION: 8-299-128
NAME/KEY: allele
LOCATION: 204138
OTHER INFORMATION: 8-296-213
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OTHER INFORMATION: 5
NAME/KEY: allele
                                                                              NAME/KEY: allele
LOCATION: 206064
OTHER INFORMATION: &
NAME/KEY: allele
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OTHER INFORMATION: 9
NAME/KEY: allele
LOCATION: 173358
OTHER INFORMATION: 9
NAME/KEY: allele
                                               LOCATION: 206545
OTHER INFORMATION:
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LOCATION: 204934
OTHER INFORMATION:
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OTHER INFORMATION: 99-5919-215 : polymorphic base A o NAME/KEY: allele
LOCATION: 197163
OTHER INFORMATION: 99-24658-410 : polymorphic base A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: allele
LOCATION: 160640
OTHER INFORMATION: 99-24639-163 : polymorphic base A or
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OTHER INFORMATION: 99-31960-363 : polymorphic base A or NAME/KEY: allele
LOCATION: 107281
OTHER INFORMATION: 99-24656-260 : polymorphic base A or OTHER INFORMATION: 99-24656-260 : polymorphic base A or
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NAME/KEY: allele
LOCATION: 8316
OTHER INFORMATION: 99-27943-150 : polymorphic base G
                                                                                                                                                 LOCATION: 205329
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 204605
OTHER INFORMATION: 8-252-190
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LOCATION: 200778
OTHER INFORMATION: 8-303-235
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OTHER INFORMATION:
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 OTHER INFORMATION: 8-251-322
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                                    Sequence 254, Application Patent No. 6444799
GENERAL INFORMATION:
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Best Local
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OTHER INFORMATION:
NAME/KEY: allele
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LOCATION: 209123
OTHER INFORMATION:
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OTHER INFORMATION: 8-278-289
NAME/KEY: allele
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OTHER INFORMATION:
NAME/KEY: allele
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
NAME/KEY: allele
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OTHER INFORMATION:
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LOCATION: 210964
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LOCATION: 210879
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OTHER INFORMATION:
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OTHER INFORMATION: 8-285-319
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LOCATION: 208285
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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APPLICANT: Ross, Bru
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                    135178
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                                                                                                                                    TTCTATTTCTTGCCTC 135163
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                           Bruce C
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             GINGIVALIS NUCLEOTIDES AND USES THEREOF
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Pred. No.
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Query Match
Best Local Similarity
Matches 15; Conserve
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US-09-252-991A-51/c
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US-09-221-017B-254
Sequence 51, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 920 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 650-813-5600
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE:
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COPTWARE: FASTSEQ for Windows Version 2.0b
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION
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                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
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100.0%; Pr
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Pred. No.
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; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/09
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 51
; LENGTH: 957
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; PERATURE:
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
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NAME/KEY: unsure
LOCATION: (102)
OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1108: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/085,598
APPLICATION NUMBER: 60/085,598
APPLICATION NUMBER: 60/051571
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE,DOCKET NUMBER: GTC-012
TELEPHONE: (781)893-5007
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Unn-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02354
COMPUTER READABLE FORM:
                                              FEATURE:
                                                                                   ORIGINAL SOURCE:
                                                                                                      TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO ANTI-SENSE: NO
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                                                                                                                                                                                   LENGTH: 975 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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SOFTWARE: ASCII
NAME/KEY: misc feature LOCATION: (B) LOCATION 1...975
                                                                  ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                           TELEFAX: (781)893-8277
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; Pred. No.
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84;
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APPLICANT: Matthews, Helena
APPLICANT: Mathews, Helena
APPLICANT: Mathews, Helena
APPLICANT: Keller, Karen
APPLICANT: Keller, Karen
APPLICANT: Wegner, Ry
TITLE OF INVENTION: Development of Resistance to Ras
TITLE OF INVENTION: Bushy Dwarf Virus
TITLE OF INVENTION: Bushy Dwarf Virus
FILE REFERENCE: 4257-0024.31
CURRENT APPLICATION NUMBER: US/09/784,508
CURRENT FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/737,719
PRIOR APPLICATION NUMBER: US 60/171,018
PRIOR FILING DATE: 1909-01-25
NUMBER OF SEQ ID NOS: 16
COFFMADE: Easter 620 10 NOS: 16
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US-09-784-508-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: modified movement protein coding sequence RBDVM4 US-09-784-508-16
                                                                                                                                                                                                                                                                                                                                                                                        US-09-784-508-3
                                                                                                                                                                                                                                                                                                                            Sequence 3, Applicat:
Patent No. 6548742
GENERAL INFORMATION:
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Patent No. 6548742
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3
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Best Local Similarity
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CURRENT FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 99/737,719
PRIOR FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: US 60/171,018
PRIOR FILING DATE: 1999-01-25
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kellogg, Jill A.
APPLICANT: Wagner, Ry
TITLE OF INVENTION: Development of Resistance to Raspberry
TITLE OF INVENTION: Bushy Dwarf Virus
FILE REFERENCE: 4257-0024.31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Mathews, Heather Raren
APPLICANT: Keller, Karen
TOANT: Kellar, Karen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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Pred. No.
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Pred. No.
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; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-2461
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US-09-697-367-7/c
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                                                                                                                                                                                                                  FILE REFERENCE: BB1166 US NA
CURRENT APPLICATION NUMBER: US/09/697,367
CURRENT TILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: 60/084,529
PRIOR FILING DATE: 1998-MAY-07
PRIOR PPLICATION NUMBER: PCT/US99/09865
PRIOR FILING DATE: 1999-MAY-06
NUMBER OF SEQ ID NOS: 24
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APPLICANT: GATY L. Breton et al.
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09697367 Patent No. 6323015
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Patent No. 6562958
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Best Local Similarity
                                                                                                                                                                                       SEQ ID NO 7
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APPLICANT:
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                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tarczynski, Mitchell
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE
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                                                                                                                                LENGTH: 1611
TYPE: DNA
ORGANISM: Zea mays
                                                                                 NAME/KEY: unsure LOCATION: (14)
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                                                                     VAME/KEY:
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(1469)
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unsure
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100.0%; Pred. No.
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Pred. No.
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84;
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Best Local :
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         Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 60/027
APPLICATION UNMBER: 60/027
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,89
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LOCATION: (1515)
NAME/KEY: unsure
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OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
CURRENT TONTION NUMBER: US/08/936,165A
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MEDIUM TYPE: Diskette
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                          TOPOLOGY: 1: MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 24-SEP-1997
                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                            ENGTH:
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Reichard, Richard
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Lonetto, Michael
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6.6%; Sur
100.0%; Pr
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Polypeptides and Their Uses
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         Score 15; DB; Pred. No. 86
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                                           DB 4;
86;
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86;
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                                                                Length 1886;
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US-08-934-494-5/c
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US-08-933-821-16/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                            Sequence 5, Application US/08934494 Patent No. 6030831
                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Gurney,
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc.
                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                              STREET: 1 DNA way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 6.6%;
Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 2042 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 536
                                                                     COUNTRY:
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STREET: 1 DNA Way
CITY: South San Francisco
                                                                                                                                          DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                   640 GATTTTCTATTTCTT 626
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                                                                                                                                          Genentech, Inc
                                                                                                                                                                            Tie Ligands
15
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Query Match
Best Local Similarity
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                                                                                               TELEPAX: 650/y52-vvv TELEPAX: 650/y52-vvv TELEPAX: 650/y52-vvv TERISTICS: SEQUENCE CHARACTERISTICS: LENGTH: 2042 base pairs TYPE: Nucleic Acid
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                                                                              US-08-960-507-16
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                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P113
TBLECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2042 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
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                                                                                            STRANDEDNESS:
TOPOLOGY: Li
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STRANDEDNESS: Single
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ADDRESSEE: Ge...
ADDRESSEE: Ge...
San Francisco
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CLASSIFICATION: 435
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             6.6%; Score 15; DB ilarity 100.0%; Pred. No. 86 Conservative 0; Mismatches
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                                                                                             Linear
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                              DB 3;
                                         Length 2042;
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               Indels
               0;
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640 GATTTTCTATTTCTT 626

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GATTTTCTATTTCTT 124

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Sequence 5, Application US/09143707
Patent No. 6348350
GENERAL INFORMATION:
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 15
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US-09-143-068-5/c
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APPLICANT: Goddard, Audrey
APPLICANT: Godwski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth
APPLICANT: Williams, Mickey
TITLE OF INVENTION: Tie Ligand Homologues
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/143,068
FILING DATE: 28-Aug-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P10
                CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2042 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: Linear
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                                                                                                                                                                                                                                                              640 GATTTTCTATTTCTT 626
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15; Conserv
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3: Genentech, Inc.
1 DNA Way
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100.0%; Pr
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; NUMBER OF SEQ ID NOS: 1', SEQ ID NO 5; LENGTH: 2042; TYPE: DNA; ORGANISM: Homo sapiens US-09-202-089-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/09202089 Patent No. 6348351
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                                                   Best
                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/202,089
CURRENT FILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: PCT/US98/19094
PRIOR FILING DATE: 1998-09-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2042 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P107
TELECOMMUNICATION INFORMATION:
TELECHEONE: 650/225-3216
                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1997-09-19
                                                                                                                                                                                                                                                                                             FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                          APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth
APPLICANT: Williams, Mickey
TITLE OF INVENTION: Tie Ligand Homologues
FILE REFERENCE: P1078P2(e)
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/143,707
FILING DATE: 28-Aug-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: South San Francisco
STATE: California
                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
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   110 GATTTTCTATTTCTT 124
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                                   l Similarity
15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                        Ferrara, Napoleone
Goddard, Audrey
Godowski, Paul J.
                                                                                                                                                                                                                                                                                                                                                                                                                         Fong, Sherman
                                                                                                                                                                                                                                                                                                                                                                                                                                         Genentech Inc.
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                                   Conservative
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                            6.6%; bu
100.0%; Pr
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100.0%; Pred. No. 86;
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                                                Score 15; pred. No.
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                                    Mismatches
                                              DB 4;
86;
                                   0,
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                                                                 Length 2042;
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RESULT 35 US-09-136-828-16/c

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS:
LENGTH: 2042 base pairs
TYPE: Nucleic Acid
STRANDENNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; P
Marches 15; Conservative 0;
                                                                                                                                                                                                                                                                                                                                         Sequence 16, Application US/09332928A Patent No. 6368853 GENERAL INFORMATION:
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Patent No. 6350450
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Gliger R.
REGISTRATION UNMBER: 33,055
REFERENCE/DOCKET NUMBER: P113
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEPAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: ITAM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPLICANT: Godowski, Paul J.
PPLICANT: Gurney, Austin L.
ITLE OF INVENTION: Tie Ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/136,828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: South San Francisco
STATE: California
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           ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                            Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                       APPLICANT: Godowski, Paul J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             640 GATTTTCTATTTCTT 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 GATTTTCTATTTCTT 124
                                                                                                                                                                                     STREET: 1 DNA Way
CITY: South San Francisco
                                                                                                                                                                   STATE: California
APPLICATION NUMBER: US/09/332,928A
                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                          ADDRESSEE: Genentech, Inc
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100.0%; Pred. No.
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86;
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-511-133-5
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                                                                                                                                                                          RESULT 38
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                                                                                                                                                          US-09-136-801-16/c
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APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
FILE REFERENCE: P1078R1C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09511133
Patent No. 6372491
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TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2042 base pairs
TYPE: Nucleic Acid
STRANDENNESS: Single
TOPOLOGY: Linear
TOPOLOGY: Linear
                                                                                                     Patent No. 6413770
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 5
LENGTH: 2042
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                                                                                                                                        Sequence 16,
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CURRENT FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: US 09/143,707
PRIOR FILING DATE: 1998-08-28
PRIOR APPLICATION NUMBER: US 60/059,352
PRIOR PILING DATE: 1997-09-19
NUMBER OF SEQ ID NOS: 15
                APPLICANT:
                                                                     APPLICANT:
APPLICANT:
                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                Local Similarity
nes 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/933,821
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                               110 GATTTTCTATTTCTT 124
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                                                                                                                      5, Application US/09136801
6413770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 14-Jun-1999 CLASSIFICATION: <Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.6%; Score 15; DB 4; ilarity 100.0%; Pred. No. 86; Conservative 0; Mismatches
                Botstein, David
Goddard, Audrey
                                                 Gurney, Austin
Hillan, Kenneth
Roy, Margaret
                                                                                                                                                                                                                                                                                                  Conservative
                                                                                     Godowski, Paul
                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                   6.6%; Score 15; DB 4; Length 2042; L00.0%; Pred. No. 86;
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PPLICANT:

Ferrara, Napoleone

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES:
CORRESPONDENCE SITE
                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3316
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APPLICANT: Schwall, Ralph
TITLE OF INVENTION: Tie Ligand Homologues
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 2042 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                 APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                              STREET: 1 DNA Way
CITY: South San Francisco
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                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 GATTTTCTATTTCTT 124
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 08/933,821
                                                                     US/09/332,929
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Sequence 5, Application US/09511631
Patent NO. 6455496
GENERAL INFORMATION:
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
FILE REFERENCE: P1078R1D1
CURRENT APPLICATION NUMBER: US/09/511,631
CURRENT APPLICATION NUMBER: US 09/143,707
PRIOR APPLICATION NUMBER: US 09/143,707
PRIOR APPLICATION NUMBER: US 09/143,707
PRIOR APPLICATION NUMBER: US 09/143,707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5
LENGTH: 2042
TYPE: DNA
ORGANISM: Homo sapiens .
US-09-690-169-5
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US-09-690-169-5/c
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                                                                                                                                                                                                                                                                   US-09-511-631-5/c
                                                                                                                                                                                                                                                                                   RESULT 41
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Gurney, Austin
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Patent No. 642621
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SEQUENCE CHARACTERISTICS:
LENGTH: 2042 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/143,707
PRIOR TILING DATE: 1998-08-28
PRIOR APPLICATION NUMBER: 60/059,352
PRIOR FILING DATE: 1997-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: GENENT.58A2D2
CURRENT APPLICATION NUMBER: US/09/690,169
CURRENT FILING DATE: 2001-09-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: TIE LIGANDS
PRIOR FILING DATE: 1997-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Dreger, Ginger R.
REGISTION NUMBER: 33,055
REGISTION NUMBER: 91:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
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nes 15; Conserv
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                                                                                                                                                                                                                                                                                                                                             640 GATTTTCTATTTCTT 626
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 15; pred. No.
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NOS: 15

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RESULT 43
US-09-630-189-5/c
; Sequence 5, Application US/09690189
; Patent No. 6521234
; GENERAL INFORMATION:
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SEQ ID NO 5
                                                                                                                                                                                                                                                        TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS:
LENGTH: 2042 base pairs
TYPE: Nucleic Acid
STRANDENNESS: Single
                                                                                                                                                                 Query Match 6.6%; Score 15;
Best Local Similarity 100.0%; Pred. No.
Matches 15; Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6492331
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Best Local Similarity
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TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                   NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/333,075
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/933,821
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winfeatin (Genentech)
CURRENT APPLICATION DATA:
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STATE: California
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                                                                                                                                                                                                                                              Linear
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RESULT 45
US-09-33-077-16/c
US-09-33-077-16/c
; Sequence 16, Application US/09333077
; Patent No. 6586397
; GENERAL INFORMATION:
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Best Local Similarity
Matches 15; Conserva
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-690-189-5
                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-202-088A-16
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APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
FILE REFERENCE: P1078R1D3
CURRENT APPLICATION NUMBER: US/09/690,189
CURRENT FILLING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: US 09/143,707
PRIOR APPLICATION 1998-08-28
NUMBER OF CON 17 NOT 1
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APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: General
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 16
LENGTH: 2042
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                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: P113093US
CURRENT APPLICATION NUMBER: US/09/202,088A
CURRENT FILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: PCT/US98/19093
PRIOR FILING DATE: 1998-09-14
NUMBER OF SEQ ID NOS: 35
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Goddard, Audrey APPLICANT: Godowski, Paul
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APPLICANT: Schwall, Ralph
TITLE OF INVENTION: TIE LIGAND HOMOLOGUES
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Hillan, Kenneth
Botstein
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Ferrara, Napoleone
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100.0%; Pred. No.
/ative 0; Mismatci
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Pred. No.
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CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 9408

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER READABLE FORM:
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COMPUTER SYSTEM:
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Result
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Maximum DB
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                Score
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seq length: 2000000000
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

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8: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

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16: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

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18: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

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                                        Sequence 12566, A
Sequence 302898,
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Sequence 195212,
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Sequence 199346,
Sequence 199347,
Sequence 199347,
Sequence 11, Appl
Sequence 11, Appl
Sequence 23845, A
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Sequence
11, Appl
18845, A
23845, A
25921, A
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-796-692- -057-475E -154-884E	-10-154-884B-345 -10-040-862-3452	-09-796-692- -10-057-475E	-10-033-528 -10-040-739	US-09-920-300A-1718 US-10-099-926-1718	-10-242-	US-09-818-656A-3 US-10-216-441-3	-10-242-515-319	9-7	-10-242-515-319	US-10-0/4-045-70	09-764-891-7	-10-037-270-	-10-117-722-	-191-997	09-815-242-7	-10-027-632-	-10-027-632-	-10-027-632-14957	-10-027-632-1	-656A-9	US-09-818-656A-94
e 2901, e 2901, e 2901,	o o	e 3452, e 3452,		• •	e 29962,	Sequence 3, Appli Sequence 3, Appli	e 3198,	Sequence 3198, Ap	e 3194	Sequence 70, Appr Sequence 3194, Ap	e 7122	e 916,	e 916,	e 130,	7429,	æ	e 1	e L	e L	e 95, Apr	Sequence 94, Appl

ALIGNMENTS

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US-09-918-995-12566/c

Sequence 12566, Application US/09918995

Publication No. US20030073623A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OB:

TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT APPLICATION NUMBER: US/09/918,995

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20

NUMBER: US/09/235,076
                                                                                                                                               ; ORGANISM: Homo sapiens; FEATURE; NAME/KEY: misc_feature; LOCATION: (1)... (476); OTHER INFORMATION: n = A,T,C US-09-918-995-12566
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                                 S
                                                                       Query Match
Best Local S
Matches 18
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                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 38054
                                                                                                                                                                                                                                                                 LENGTH: 476
TYPE: DNA
110
                                   38
                                                                       l Similarity
18; Conserv
                   ATTTTTGATGGCCTTAAG
ATTTTTGATGGCCTTAAG
                                                                   7.9%; So lilarity 100.0%; I conservative 0;
93
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                                                                                         Score 18; DB 11; Length 476; Pred. No. 14;
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                                                                       Gaps
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RESULT 2
US-10-027-632-302898/c
; Sequence 302898, Application US/10027632
; Publication No. US20030204075A9

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US-10-027-632-302898
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US-10-027-632-302898/c
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PRIOR PILING DATE: 2000-07-12
PRIOR PELICATION NUMBER: US 60/198,676
PRIOR FILLING DATE: 2000-04-20
PRIOR FILLING DATE: 2000-03-29
PRIOR PELICATION NUMBER: US 60/193,483
PRIOR PELICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILLING DATE: 1999-09-28
PRIOR FILLING DATE: 1999-09-28
PRIOR FILLING DATE: 1999-09-28
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        Matches
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
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CURRENT FILING DATE: 2002-04-30
                                                                                                                                 LENGTH: 47
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TYPE: DNA
ORGANISM: Human
                                                                                                         ORGANISM: Human
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/193,483 FILING DATE: 2000-03-29 APPLICATION NUMBER: US 60/185,218 FILING DATE: 2000-02-24 APPLICATION NUMBER: US 60/167,363 FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/156,358
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      18; Conservative
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                            Similarity
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100.0%; Pr.
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    7.9%; Score 18; DB
100.0%; Pred. No. 14;
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                       DB 14;
14;
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; TYPE: DNA
; ORGANISM: Human
US-10-027-632-195212
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CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR PILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23
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SOFTWARE: FastSEQ for
SEQ ID NO 195212
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 195212, Apgeneral INFORMATION
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
                                                                                                                                                      PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                   PRIOR FILING DATE: 1999-09-28
                                                                       PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
                                                                                                     PRIOR APPLICATION NUMBER: US 60/167,363 PRIOR FILING DATE: 1999-11-23
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APPLICATION NUMBER: US 60/146,002 FILING DATE: 1999-08-09
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100.0%; Pred. No.
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US-10-027-632-199346/c
; Sequence 199346, Application US/10027632
; Publication No. US20030204075A9
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Best Local S
Matches 18
                                                                                                                                                                                   Sequence 199347, Application US/10027632 Publication No. US20030204075A9 GENERAL INFORMATION:
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 195212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 199346
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PRIOR TILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
COPPERATOR
              CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
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TYPE: DNA
ORGANISM: Human
                                                                                                           APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
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CURRENT FILING DATE: 2002-04-30
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FILING DATE: 2000-04-20
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Pred. No.
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Pred. No
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US-10-027-632-199346/c
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                                                                                                                                                ; ORGANISM: Human US-10-027-632-199346
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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 199347
                                                                                                                                                                                                                        SOFTWARE: FastSI
SEQ ID NO 199346
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                                                                         Matches
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Best Local Similarity
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
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                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
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PRIOR APPLICATION NUMBER: US 60/156,358
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                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/185,218 PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                     TYPE: DNA
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                                    ATAAAGCACTCAATTTCT 29
ATAAAGCACTCAATTTCT 448
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Pred. No.
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Pred. No.
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RESULT 9
US-10-027-632-199347/c
Sequence 199347, Application US/10027632
GENERAL INFORMATION:

APPLICANT: Wang, David G.

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RESULT 11
US-09-918-995-18845/c
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; ORGANISM: Homo sapiens
US-10-428-487-11
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US-10-428-487-11/c
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US-10-027-632-199347
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR TILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
Sequence 18845, Application US/09918995 Publication No. US20030073623A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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Best Local Similarity 100.0%;
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PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/428,487
CURRENT FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: 09/815,153
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,201
PRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: GERBER, HANS-PETER
TITLE OF INVENTION: VEGF-MODULATED GENES AND METHODS EMPLOYING
FILE REFERENCE: 09800080-0103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: RASTELLI, LUCA K. APPLICANT: GERBER, HANS-PET
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100.0%; Pred. No.
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBY
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE; 2041-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 18845
LENGTH: 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ChondroGene Inc.

APPLICANT: Liew, C.C.

APPLICANT: Liew, C.C.

PITLE OF INVENTION: Compositions and Methods Relating to FILE REFERENCE: 4231/2005

CURRENT APPLICATION NUMBER: US/10/242,535A

CURRENT FILING DATE: 2002-09-12

PRIOR APPLICATION NUMBER: US 10/085,783

PRIOR FILING DATE: 2002-02-28

PRIOR FILING DATE: 2002-02-34

PRIOR FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 60/305,340

PRIOR APPLICATION NUMBER: US 60/305,340

PRIOR APPLICATION NUMBER: US 60/305,017

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR APPLICATION NUMBER: US 60/275,017
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US-10-242-535A-25921
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                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-23845
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                                                              Sequence 25921, Application US/10242535A Publication No. US20040013663A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 17; Conserv
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Best Local !
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APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 58994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
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NAME/KEY: misc_feature

LOCATION: (1)...(378)

OTHER INFORMATION: n = A,T,C or
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FILE REFERENCE: 4231/2005

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CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
VUMBER OF SEQ ID NOS: 58994
SOFTWARE: PATENTIN VETSION 3.2
SEQ ID NO 25921
LENGTH: 450
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Sequence 310795, Application US/10027632
Publication No. US20030204075A9
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                                                                                                                                                                                                                                                              FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FPILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
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LOCATION: (291)...(291)
OTHER INFORMATION: n is a,
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OTHER INFORMATION: n is
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OTHER INFORMATION: n is
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LOCATION: (283)..(283)
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OR APPLICATION NUMBER: US 60/193,483
OR FILING DATE: 2000-03-29
OR APPLICATION NUMBER: US 60/185,218
OR FILING DATE: 2000-02-24
OR APPLICATION NUMBER: US 60/167,363
OR APPLICATION NUMBER: US 60/167,363
OR FILING DATE: 1999-11-23
OR APPLICATION NUMBER: US 60/156,358
OR APPLICATION NUMBER: US 60/146,002
OR APPLICATION NUMBER: US 60/146,002
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17; Conserva
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FILE REFERENCE: CL001191
CURRENT APPLICATION NUMBER: US/09/818,656A
CURRENT FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 103
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 94

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; TYPE: DNA
; ORGANISM: Human
US-10-027-632-310795
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                                                                                                                                       US-09-818-656A-94
Sequence 94, Application US/09818656A
Patent No. US20020142381A1
GENERAL INFORMATION:
APPLICANT: GONG, Fangcheng et al.
TITLE OF INVENTION: ISOLATED HIMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 310795
LENGTH: 581
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GENERAL INFORMATION
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SEQ ID NO 310795
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Best Local
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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CURRENT FILING DATE: 2002-04-30
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17; Conserv
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17; Conserv
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Pred. No.
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Pred. No.
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-818-656A-94
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; SEQ ID NO 95
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-818-656A-95
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APPLICANT: Wang, David G.
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 149573, Application US/10027632 Publication No. US20030204075A9
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SEQ ID NO 149573
LENGTH: 724
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Best Local
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TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001191
                                                        PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
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CURRENT FILING DATE: 2002-04-30
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                                          SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                   APPLICATION NUMBER: US 60/193,483 FILING DATE: 2000-03-29 APPLICATION NUMBER: US 60/185,218 FILING DATE: 2000-02-24
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17; Conserv
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17; Conservative
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Pred. No.
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
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PRIOR FILING DATE: 1999-11-23
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nes 17; Conserv
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NUMBER: US 60/167,363
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Pred. No.
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Pred. No.
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GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
Trawick, John D.
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US-09-815-242-7429/c
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US-10-027-632-149574
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US-10-027-632-149573
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                       Sequence 7429, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEO ID NO 149573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2000-04-20
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TYPE: DNA
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FILING DATE: 2000-03-29
APPLICATION NUMBER: US 60/185,218
FILING DATE: 2000-02-24
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17; Conserv
                   Zyskind, Judith W. Wall, Daniel
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Pred. No.
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US-09-815-242-7429
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SEQ ID NO 130
LENGTH: 2279
TYPE: DNA
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                                                                                                                                                                                                                                                        TITLE OF INVENTION: Oligonicleotide-Containing Pharmacological Compositions And Their FILE REFERENCE: 54800-5019
CURRENT APPLICATION NUMBER: US/10/191,997
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US 60/303,820
PRIOR PILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 132
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITEA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/2106,848
PRIOR APPLICATION NUMBER: 60/206,848
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PRIOR APPLICATION NUMBER: 60/207,727
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PRIOR APPLICATION NUMBER: 60/242,578
                                                                                                                 FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: NM_001752
                                                                                                                                                                       ORGANISM: Homo sapiens
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27 TCTACTCAGAAATTTTT 43
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17; Conserv
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DALE, Roderic M.
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o. US20030207834A1
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PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 916
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Best Local Similarity 100.0%;
Matches 17; Conservative (
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (103)..(1686)
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TITLE OF INVENTION: NO. US20030219744A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2BCIP
CURRENT APPLICATION NUMBER: US4010/117,722
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: 09/620,312
PRIOR FILING DATE: 2000-07-19
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
                                                     APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: Tillinghast, John
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030104529Alel Nucleic Acids
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
                   CURRENT APPLICATION NUMBER: US/10/037,270
CURRENT FILING DATE: 2002-01-04
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APPLICATION NUMBER: 09/552,317
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Zhang, Jie
Ren, Feiyan
                                                                                                                                                                                                                                                                                                    Zhao,
                                                                                                                                                                                                                               Wang,
                                                                                                                                                                                                                                             Xue, Aidong J.
Yang, Yonghong
                                                                                                                                                                                                                                                                                                                      Chen, Rui-hong
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b. US20030219744A1
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nan, Tom
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100.0%; Pred. No.
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PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: pt FL-genes Version 1.0
SEQ ID NO 916
LENGTH: 2318
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (103)...(1686)
US-10-037-270-916
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-7122
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                                                                          ; ORGANISM: Homo sapiens
US-10-074-045-70
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Publication No. US20030092102A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 17; Conserv
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NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7122
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Best Local
Query Match 7.5%;
Best Local Similarity 100.0%;
Matches 17; Conservative
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ21C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
                                                                                                                                                                               Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 74
                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/074,045
CURRENT FILING DATE: 2002-02-14
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                                                                                                           LENGTH: 18657
TYPE: DNA
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17; Conserv
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00.0%; Pred. No.
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   Score 17; DB; Pred. No. 64, 0; Mismatches
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Pred. No.
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56;
                                     Length 18657;
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; SEQ ID NO 3194
; LENGTH: 28313
; TYPE: DIA
; ORGANISM: Homo sapiens
US-09-764-877-3194
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US-09-764-877-3194/c
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
               SOFTWARE: Paten
SEQ ID NO 3194
LENGTH: 28313
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CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
                                                                             Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 4031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/242,515
CURRENT FILING DATE: 2002-09-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/180,628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
TYPE: DNA
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                                                                                                                     APPLICATION NUMBER: 60/218,290 FILING DATE: 2000-07-14
                                                                                                                                                                                                   FILING DATE: 2000-07-26
APPLICATION NUMBER: 60/217,496
FILING DATE: 2000-07-11
                                                                                                                                                                                                                                                               FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/220,963
                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-07-11
APPLICATION NUMBER: 60/225,758
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                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/217,487
                                                                                                                                                                               APPLICATION NUMBER: 60/225,447
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                                                         PatentIn Ver.
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Pred. No.
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                                                                                                File Wrapper or
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; ORGANISM: Homo sapiens
US-09-764-877-3198
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US-09-764-877-3198/c
                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/242,515
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: 09/764,877
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
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Best Local Similarity
Matches 17; Conserv
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 4031
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3198
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Publication No. US20040009488A1
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CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
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                                                                           PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-07-14
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TITLE OF INVENTION: Nucleic Acids, Proteins,
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                                                                                               FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/218,290
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100.0%; Pred. No.
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Pred. No.
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GENERAL INFORMATION:

APPLICANT: GONG, FANGCHENG et al

TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: CLUO1191CON

CURRENT APPLICATION NUMBER: US/10/216,441

CURRENT PILING DATE: 2002-08-12

PRIOR APPLICATION NUMBER: 09/818,656

PRIOR FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FASESEQ for Windows Version 4.0

SEQ ID NO 3
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US-10-242-515-3198
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                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo spaiens
US-10-216-441-3
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US-10-216-441-3
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Patent No. US20020142381A1
GENERAL INFORMATION:
APPLICANT: GONG, FANGCheng et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REPERENCE: CL001191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                             Query Match
Best Local :
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 40645
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nes 17; Conservative
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36001 TTTCTATTTCTTGCCTC 36017
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                                                                               Similarity
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                               TTTCTATTTCTTGCCTC 129
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                                                          100.0%; F1
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                                                              score 17; DB; Pred. No. 67; 0; Mismatches
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65;
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67;
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RESULT 34

RESULT 36 US-10-099-926-1718/c ; Sequence 1718, Application US/10099926

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APPLICANT: Chondrogene Inc.

APPLICANT: Liew, C.C.

APPLICANT: Liew, C.C.

FITTLE OF INVENTION: Compositions and Methods Relatiing to FILE REFERENCE: 4231/2005

FILE REFERENCE: 4231/2005

CURRENT APPLICATION NUMBER: US/10/242,535A

CURRENT FILING DATE: 2002-09-12

PRIOR APPLICATION NUMBER: US 10/085,783

PRIOR FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: US 60/305,340

PRIOR APPLICATION NUMBER: US 60/305,340

PRIOR APPLICATION NUMBER: US 60/305,340

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-12
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US-10-242-535A-29962
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                                                                                                                                                                                                                                                                                    FILE REFERENCE: 210121.547
CURRENT APPLICATION NUMBER: US/09/920,300A
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 1789
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1718
LENGTH: 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1718, Application Patent No. US20020136728A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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Best Local
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APPLICANT: Meagher, Madeleine Joy
APPLICANT: Xu, Jistngchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 58994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/271,955 PRIOR FILING DATE: 2001-02-28
                                                                                                                                                                     FEATURE:
NAME/KEY: misc feature
NAME/KEY: misc feature
LOCATION: 29, 215, 242, 257
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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134
                                    189 CTCACCTCCGTCCCTC 204
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16; Conserv
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Pred. No.
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Pred. No.
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1.7e+02;
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RESULT 38
US-10-040-739-1242/c
US-10-040-739-1242/c
; Sequence 1242, Application US/10040739
; Publication No. US20020173635A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                         ; NAME/KEY: misc_feature
; LOCATION: 29, 215, 242, 257
; OTHER INFORMATION: n = A,T,C or
US-10-033-528-1718
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; LOCATION: 29, 215, 242, 257
; OTHER INFORMATION: n = A,T,C or G
US-10-099-926-1718
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1718
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CURRENT FILING DATE: 2002-03-17
NUMBER OF SEQ ID NOS: 1992
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1718
LENGTH: 287
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Best Local Similarity
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APPLICANT: Meagh
APPLICANT: Xu, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Secriet, Heather TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER FILE REFERENCE: 210121.547C1
CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT FILING DATE: 2001-12-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Publication No. US20030166064A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: King, Gordon B.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
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APPLICANT: Secrist, Heather
APPLICANT: Jiang, Yuqiu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547C2
                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 287
TYPE: DNA
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100.0%; Pred. No.
tive 0; Mismatc
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Pred. No.
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1.7e+02;
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RESULT 39
US-09-796-692-3452/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                         APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR APPLICATION NUMBER: 60/190,479
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MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
APPLICATION NUMBER: US/10/040,739
PILING DATE: 07-Jan-2002
CLASSIFICATION - CURKNOWN>
PRIOR APPLICATION NUMBER: 09/036,520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                       APPLICATION NUMBER: 60/200,545
FILING DATE: 2000-04-27
APPLICATION NUMBER: 60/200,303
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MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1242:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Merberg, David
Treacy, Maurice
Spaulding, Vikki
TITLE OF INVENTION: SECRETED,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTATAAAGCACTCAA 188
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Massachusetts COUNTRY: U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Cambridge
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STREET: 87 CambridgePark Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LaVallie,
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: (617) 8:
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; Pred. No. 1.8e+02;
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FILING DATE: 2000-04-28
APPLICATION NUMBER: 60/200,779
FILING DATE: 2000-04-28

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Matches
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SOFTWARE: FRACTSEQ for Windows Version 3.0
SEQ ID NO 3452
LENGTH: 422
TYPE: DNA
ORGANISM: Homo Bapiens
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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Publication No. US20040002068A1
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                                                                APPLICANT: Ordonez, Nadia
APPLICANT: Carter, Lauren
APPLICANT: McNeill, Patricia Dianne
APPLICANT: McNeill, Patricia Dianne
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-014402US
CURRENT APPLICATION NUMBER: US/10/057,475B
CURRENT FILING DATE: 2002-01-22
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PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
                                                                                                                                                                                                                                                                                                      APPLICANT: Gaiger, Alexander
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OTHER INFORMATION:
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LOCATION: (356)
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LOCATION: (340)
OTHER INFORMATION:
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LOCATION: (151)
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RR FILLING DATE: 2000-05-22
DR APPLICATION NUMBER: 60/218,950
DR FILLING DATE: 2000-07-14
DR APPLICATION NUMBER: 60/222,903
DR FILLING DATE: 2000-08-03
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FILING DATE: 2000-05-01
APPLICATION NUMBER: 60/202,084
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APPLICATION NUMBER: 60/223,378
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16; Conserva
                                                                                                                                                                                                                            Mannion, Jane
Clapper, Jonathan David
Wang, Aijun
                                                                                                                                                                                                                                                                                    Algate, Paul A.
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hes 0;
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                                                                                                                                            the Detection,
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RESULT 41
US-10-154-884B-3452/c
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CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
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NUMBER OF SEQ ID NOS: 10979
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                       PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gaiger, Alexander APPLICANT: Algate, Paul A. APPLICANT: Mannion, Jane APPLICANT: Retter, Marc W.
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TYPE: DNA
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OTHER INFORMATION: n = g, a, c or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OR FILING DATE: 2000-05-01
OR FILING DATE: 2000-05-01
OR APPLICATION NUMBER: US 60/202,084
OR FILING DATE: 2000-05-04
OR APPLICATION NUMBER: US 60/206,201
OR APPLICATION NUMBER: US 60/206,201
OR FILING DATE: 2000-05-22
OR APPLICATION NUMBER: US 60/218,950
OR APPLICATION NUMBER: US 60/222,903
OR APPLICATION NUMBER: US 60/222,903
                                         PAPPLICATION NUMBER: US 6
FILING DATE: 2000-05-04
APPLICATION STATE: 2000-05
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FILING DATE: 2000-04-28
APPLICATION NUMBER: US 60/200,779
FILING DATE: 2000-04-28
                                                                                                                       APPLICATION NUMBER: US 60/202,084
                                                                                                                                            FILING DATE:
                                                                                                                                                                                APPLICATION NUMBER: US 60/200,779 FILING DATE: 2000-04-28
                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/200,303 FILING DATE: 2000-04-28
                                       APPLICATION NUMBER: US 60/218,950
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Retter, Marc W.
Corixa Corporation
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: 2000-07-14
NUMBER: US
                                                                                                                                            2000-05-01
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  60/222,903
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Pred. No.
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. 1.8e+02;
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                                                                                                                   SOFTWARE: Fast
SEQ ID NO 3452
LENGTH: 422
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3452
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Publication No. US20030078396A1
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Best Local Similarity
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TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:

NAME/KEY: misc feature
LOCATION: (1)...(422)

OTHER IMPORMATION: n = 9, a
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TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
                                                                                                                                                          NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/040,862 CURRENT FILING DATE: 2001-11-06 PRIOR APPLICATION NUMBER: US 60/186,126 PRIOR FILING DATE: 2000-03-01 PRIOR APPLICATION NUMBER: US 60/190,479 PRIOR FILING DATE: 2000-03-17
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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
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PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
NAME/KEY: unsure
LOCATION: (151)
OTHER INFORMATION: n=A,T,C or G
                                                           TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                   APPLICATION NUMBER: US 09/796,692 FILING DATE: 2001-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/200,779
FILING DATE: 2000-04-28
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APPLICATION NUMBER: US 60/223,416
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APPLICATION NUMBER: US 60/218,950
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Retter, Marc
Corixa Corporation
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Pred. No.
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PRIOR FILING DATE: 2000-08-07;
PRIOR APPLICATION NUMBER: 60/223,378;
PRIOR FILING DATE: 2000-08-07;
NUMBER OF SEQ ID NOS: 9597;
SOFTWARE: FABLSEQ for Windows Version SEQ ID NO 2901
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; ORGANISM: Homo sapiens US-09-796-692-2901
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US-09-796-692-2901
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APPLICANT: Gaiger, Alexander
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Best Local Similarity 100.0%;
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APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077-001200
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR PRIOR DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2901, Application US/09796692 Publication No. US20020198362A1
                                  LENGTH: 42
TYPE: DNA
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NAME/KEY: unsure
LOCATION: (356)
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (165)
OTHER INFORMATION: n=A,T,C or
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LOCATION: (165)
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                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/222,903
                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/202,084 FILING DATE: 2000-05-04
                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/200,999
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/200,779
                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/218,950
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Pred. No. 1.8e+0
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Query Match

7.0%;

Score 16;

DB 10;

Length 427;

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FILE REFERENCE: 014058-011402US
CURRENT APPLICATION NUMBER: US/10/057,475B
CURRENT FILING DATE: 2000-01-22
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR APPLICATION NUMBER: US 60/200,094
PRIOR APPLICATION NUMBER: US 60/200,094
PRIOR APPLICATION NUMBER: US 60/200,094
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/208,990
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
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; ORGANISM: Homo sapiens
US-10-057-475B-2901
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                                                         Sequence 2901, Application US/10154884B Publication No. US20040005561A1 GENERAL INFORMATION:
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Best Local
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APPLICANT:
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                APPLICANT: Gaiger, Alexander APPLICANT: Algate, Paul A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 10979
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ordonez, Nadia
APPLICANT: Carter, Lauren
APPLICANT: McNeill, Patricia Dianne
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
APPLICANT:
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APPLICANT: Algate, Paul A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2000-07-14
APPLICATION NUMBER: US 60/222,903
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100.0%; Pred. No.
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0; Mismatches 0;
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hes 0;
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                                                                                                                                                                                                                                                                                                                                                                Length 427;
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Search completed: February
Job time : 1691 secs
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; ORGANISM: Homo sapiens
US-10-154-884B-2901
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CURRENT APPLICATION NUMBER: US/10/154,884B
CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
                                                                                                                                                                                                                                                                                                                                  Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 11290
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2901
                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR APPLICATION NUMBER: US 60/200,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Compositions and Methods for the Detection,
                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/218,950 FILING DATE: 2000-07-14
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                                                                                                                                                                      Conservative
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                     4,
                                                                                     176
                     2004, 16:36:28
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Pred. No. 1.8e+02;
                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                              Length 427;
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Minimum
Maximum
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length: 2000000000
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em_gss_pln:
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em_gss_mam:
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musculus AV341547 Mus musculus (house mouse) AV341547.1 GI:6381599

REFERENCE AUTHORS

SOURCE ORGANISM

KEYWORDS

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RESULT 1 AV341547/c LOCUS

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DEFINITION

AV341547

211 bp mRNA linear EST 11-NOV-199: RIKEN full-length enriched, adult male olfactory bulb Mus cDNA clone 6430522K10 3', mRNA sequence.

EST 11-NOV-1999

ALIGNMENTS

AV341547

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; vercondata; Muridae; Madmalia; Eutheria; Rodentia; Sciurognahi, Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishi, Y., Ishikawa, T., Itoh, M., Izawa, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Tsunoda, Y., Wataniki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

Result No.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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JOURNAL COMMENT

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Description

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URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
BU465599.1
EST.
                                                                        BU465599 389 bp 1603773567F1 CSEQRBN19 Gallus gallus
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Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carrinci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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                                                        sequence.
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/dev_stage="adult"
/lab_host="DH10B"
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/sex="male"
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|strain="C57BL/6J"
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                  GI:25955073
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Department of Biomolecular Sciences
University of Manchester Institute
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Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 389)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PO Box 88, Manchester, M60 1QD, Tel: 01612008930 Fax: 01612360409
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                 Borges, K.M., Brummet, S.R., S.T., Szasz, J., Ravel, J.,
                                                                                                                     Pyrococcus furiosus
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0299F Pyrococcus furiosus
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                                                         Thermococcaceae; Pyrococcus.
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/clone lib="CSEQRBN19"
/clone = "Organ: ovary; Vector: pBluescript II KS(+); Site_1:
/clone = "Organ: ovary; Vector: pBluescript II KS(+); Site_1:
/conet = "Organ: ovary; Vector: pBluescript II KS(+); Site_1:
/conet = "Organ: ovary; Vector: primer was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
/constructed from 1 million reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with EcoRI
/size-selected, and cloned into the NotI and EcoRI
/compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
                                                                                                                                                                                                                     394 bp mRNA rococcus furiosus 1-ZAP II library, cDNA clone 0299, mRNA sequence.
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|mol_type="mRNA"
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lab_host="DH10B"
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,J., Fuller,C., Chase,J.W.
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and Hubbard,
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Pyrococcus furiosus
Pyrococcus furiosus
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Amersham Life Science, Inc.
Amersham Life Science, 26101
Tel: 2164649277; 4102348870
Fax: 2163600975; 4102348896
                                                                                                                                          High Throughput Sequencing Center University of Washington
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Mahairas,G.G., Wallace,J.C., Smitl
Keller,A., Shaker,R., Furlong,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ207356 487 bp DNA linear GSS 18-SEP-1998 HS_3240_B1_G02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3240 Col=3 Row=N, genomic survey
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                                                                                                                                                                                                                                                                     Sequence-tagged connectors: A sequence approach to mapping scanning the human genome
                                   Plate: 3240 rov
Class: BAC ends
                                                                                                                                                                                                 Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                    Sequence Tagged Connector
                                                                                                                                                                                                                                                      scanning the human genome
Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTTTATAAAGCACTCAAT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Survey of the Genome of the Hyperthermophilic Archaeon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138
                                                                                       (206) 616-3618
(206) 616-3887
l: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.3%; Silarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens
                  quality sequence stop: 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="Pyrococcus furiosus 1-ZAP II library, F Robb"
/note="Vector: 1-ZAP II; Site 1: Eco RI; Site 2: Eco RI;
Genomic DNA was purified from P. furiosus cells and
partially digested with Dra I, Eco RV, Hinc II, Pvu II,
size selected, ligated to Eco RI linkers then cloned into
the Eco RI site of 1-ZAP II, plasmid excision vector.
Excision was performed in batch and individual clones
retrieved by plating."

93 g 107 t 6 others
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Pyrococcus
/mol_type="mRNA"
/strain="DSM 3638"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:3618561
                                                    row: N
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Pred. No.
                                                      column: 3
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                                                                                                                                             Seattle,
                                                                                                                                                                                                                                                                                                                                               Smith, K.,
                                                                                                                                                                                                                                                      96
                                                                                                                                                                                                                                                    (17),
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39;
                                                                                                                                                                                                                                                                                                                          h,K., Swartzell,S.,
Young,J., Zhao,S.,
                                                                                                                                             WA 98109,
                                                                                                                                                                                                                                                       9739-9744 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 394;
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REFERENCE
AUTHORS
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KEYWORDS
SOURCE
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BU441045
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MEDLINE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archomauria; Avee; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boardman, P. E., Sanz-Ezquerro, J., Overton, I.M., I
Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BU441045
604142968F1 CSEQRBN11 Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 01612008930
Fax: 01612360409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archosauria; Aves; Neognathae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus
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BU441045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12445392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 619)
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/lab_nost="unave"/
/clone lib="VSEQRRN11"
/clone lib="VSEQRRN11"
/note="Vector: pBluescript II KS(+); Site_1: EcoRI;
/note in the first strand in the first strand strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.3%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Simon.Hubbard@umist.ac.uk.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: sperm;
E-Coli DH10B"
a 95 c 153 g
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/strain="Layer and broiler"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                    /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="Plate=3240 Col=3 Row=N'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                         tissue_type="muscle"
                                                                                                                                                                                                                                                                                                                               sex="Male and female"
                                                                                                                                                                                                                                                                                                                                               clone="ChEST978h18"
                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:25930356
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M60 1QD,
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41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Technology (UMIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burt,D.W., Bosch,E., and Hubbard,S.J.
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Clones in
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118 5', mRNA
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hybridization was

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SOURCE
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VERSION
KEYWORDS
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BU368119
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                                                            BASE COUNT
ORIGIN
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ORIGIN
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boardman, P. E., Sanz-Ezquerro, J., Overton, I.M., I
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archosauria; Aves; Neognathae; Phasianinae; Gallus.
1 (bases 1 to 672)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22335534
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                                                                     /clone lib="CSEQCHN72"
/clone lib="CSEQCHN72"
/clone lib="CSEQCHN72"
/note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site_2: Not1; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with EcoRI
, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Simon. Hubbard@umist.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="ChEST73915"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="Compton Line
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  tissue_type="cerebrum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  significantly longer reannealing
sed."
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100.0%;
     8.3%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 type="mRNA"
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     Score 19;
Pred. No.
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Pred. No.
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19; Conserv
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BX165567
BX165567.1
GSS.
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                                                                                                                        Archosauria; Aves; Neognathae; Galliformes; Ph
Phasianinae; Gallus.
1 (Dases 1 to 679)
Herault,F., Le Meuth Metzinger,V., Desert,C.,
                                                                                                                                                                                                                                                                                                    BX263205 AGENAE Gallus gallus multi-tissues normalized and once-subtracted cDNA library (gcal) Gallus gallus cDNA clone
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INRA, UMR INRA-ENSAR Genetique Animale 65, rue de Saint-Brieuc, RENNES cedex, Tel: +33 (0) 2.23.48.54.63
                                              Contact: Douaire M
                                                             Unpublished
                                                                             Construction and primary characterization multi-tissue cDNA libraries
                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                         Gallus gallus (chicken)
Gallus gallus
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                                                                                                                                                                                                                                                                                       gcal0008c.n.07 5prim, mRNA sequence
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
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/db_xref="taxon:7955"
/clone="DKEY-124L1"
/tissue_type="Testis"
/note="vector pindigoBAC-536"
a 120 c 128 g 258 t
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/mol_type="genomic DNA"
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1 (bases) to 683)

Arakawa, T., Carninci, F., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Haramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
                                                                                                                                   Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     883 bp mRNA linear EST 26-00 BB621652 RIKEN full-length enriched, 11 days embryo head Mus musculus cDNA clone 6230413013 5', mRNA sequence.
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Seq primer: M13R.
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Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                         Unpublished
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/note="Wector: pT73D-pac; tissues: adipose tissue, brain, kidney, liver, multi-tissues, muscle, ovary, testis, bone marrow, caecum, duodenum, embryos, fabricius gland, granulosa, hypothalamus, ileon, jejunum, oviduct, pancreas, skin, spleen, thymus, utero-vaginal gland, pituitary, sakin, spleen, thymus, utero-vaginal gland, pituitary, gland, hematopoietic progenitor cells, small follicle. Clone distribution: AGENAE Resource centre. Francois PIUMI, Francois.Piumi.inra.fr, INRA, CEA Radiobiologie et Etude du genome (LEEG), Domaine de Vilvert, 78352,
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154 c 187 g
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/dev_stage="from embryos to adults"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
                                                                                                                                                                                                                                                                                                                                                                        BamHI.
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nead"
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/dev_stage="11 days embryo"
/lab_host="DH10B"
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CSEQCHN38 Gallus gallus cDNA clone ChEST657n21
GI:25513312
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                                                                                                                                                                                                                                                                                           8.3%;
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1 (bases 1 to 716)
Boardman, P.E., Sanz-Ezquerro, J., Ove
Fong, W.T., Tickle, C., Brown, W.R.A.,
                                                                                                            Gallus gallus (chicken)
Gallus gallus
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                                                      Archosauria; Aves; Neognathae; Phasianinae; Gallus.
                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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//clone lib="CSEQCHN38"
//clone lib="CSEQCHN38"
//cote="Torgan: limbs; Vector: pBluescript II KS(+); Site_1:
ECORI; Site_2: Not1; This normalized library was
constructed from 1 million independent clones: cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with ECORI
, size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-932 and Bonaldo et al., Genome Research 6
(1995): 791, except that a significantly longer
reannealing hybridization was used."
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gallus
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/lab_host="DH10B"
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/clone="ChEST657n21"
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                                                                                                                                                                   GI:25865331
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3 (comprehensive Collection of Chicken cDNAs Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (chicken)
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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Department of Biomolecular Sciences
University of Manchester Institute
                                                            Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute
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603363138F1 CSEQRBN21 Gallus
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Site 1: EcoRI; Site 2: Not1; This normalized library was
constructed from 1 million independent clones.cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with EcoRI
, size-selected, and cloned into the NotI and EcoRI
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/mol_type="mRNA"
/strain="White Leghorn, H
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/dev_stage="36"
/lab_host="DH10B"
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                                                                                                      Biomolecular Sciences
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ChEST258k9 5', mRNA
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RESULT 13
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1 (bases 1 to 770)

1 (bases 1 to 770)

1 (bases 1, to 770)

1 (bases 1, to 770)

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8 (bases 1, to 70)

9 (bases 1, to 70)

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Gallus gallus
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                                                                                                                                                                                                                                                                                                                                                                                Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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                                                                                                                                                                                                                                                                                                           PO Box 88, Manchester,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simon Hubbard
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//lab_host="DH10B"
//clone_lib="CSEQRBN21"
//clone_lib="CSEQRBN21"
//clone_lib="CSEQRBN21"
//clone_lib="CSEQRBN21"
//note="forgam: ovary; Vector: pBluescript II KS(+); Site_l:
//note="forgam: ovary; Vector: pBluescript II KS(+); Site_l:
//note="forgam: ovary; Vector: pBluescript was:
constructed from 1 million independent clones: cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with EcoRI
// size-selected, and cloned into the NotI and EcoRI
// size-selected, and cloned into the NotI and EcoRI
// size-selected, and cloned into the NotI and EcoRI
// size-selected, and cloned into the NotI and EcoRI
// compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
// (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
// (1996): 791, except that a significantly longer
// reannealing hybridization was used."
                                                                                                                                         Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simon.Hubbard@umist.ac.uk.
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/clone="ChEST258k9"
                                    /organism="Gallus gallus"
/mol_type="mRNA"
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/strain="Compton Line 151"
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cDNA clone ChEST791g16 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 787)
1 (bases 1 to 787)
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603555112F1 CSEQCHN52 Gallus gallus cDNA clone ChEST428h4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., E Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. A Comprehensive Collection of Chicken cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (chicken)
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BU268139
                                                                                                                                                                                                                                                                                                                                                                                                                       Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 01612360409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PO Box 88, Manchester, Tel: 01612008930
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//Clone lib="CSEQCHN74"
//Clone
/clone_lib="CSEQCHN52"
/note="Organ: limbs; Vector: pBluescript II KS(+); Site_1:
/note="Organ: limbs; Vector: pBluescript II KS(+); Site_1:
/note="Organ: Vector I million independent clones.cDNA"
                                                                                                                                                                                                                                            /organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
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                                                                                                                                      /clone="ChEST428h4"
/dev_stage="22"
/lab_host="DH10B"
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M60 1QD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 26-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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RESULT 15
BU446400
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ORGANISM
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
MEDLINE
PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BU446400 792 bp mRNA linear EST 29-NOV-
603213673F1 CSEQRBN13 Gallus gallus cDNA clone ChEST196b19 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 792)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (chicken)
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: Simon. Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BU446400.1 GI:25935711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PO Box 88, Manchester, M60 1QD, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12445392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01612360409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01612008930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
/note=Torgan: Ovary; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: Not1; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS
                                                                                                                                                                                                                                                                                                                                    /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                          /clone="ChEST196b19"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/strain="Layer"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                        clone_lib="CSEQRBN13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Gallus gallus"
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KEYWORDS

VERSION

FEATURES

Query Match Best Local Similarity

8.3%;

Score 19; Pred. No.

DB 13; 47;

COMMENT

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REFERENCE
AUTHORS
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BU314014
LOCUS
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KEYWORDS
BASE COUNT
ORIGIN
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ORIGIN
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MEDLINE
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Best Local
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Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 810)
1 (bases 1 to 810)
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., E Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. A Comprehensive Collection of Chicken cDNAs Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BU314014 810
603541537F1 CSEQCHN61 Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: Simon. Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Biomolecular Sciences University of Manchester Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simon Hubbard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (chicken)
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                       188
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                       þ
                                                                                                                       /note="Torgan; heart; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: Not1; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI; size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (1994) 91: 9228-9232 and Bonaldo et al., Genome (1996): 791, except that a significantly longer reannealing hybridization was used."

186 c 229 g 189 t
                 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research (1996): 791, except that a significantly longer reannealing hybridization was used."

192 c 236 g 194 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol
                                                                                                                                                                                                                                                                                                                                                                                                                        db_xref="taxon:9031"/clone="ChEST511j10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                             dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           strain="Compton Line 15I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                                                                         sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:25822015
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                                                                                                                                                                                                                                                                                                                                                           host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   type="mRNA"
                                                                                                                                                                                                                                                                                                                                        lib="CSEQCHN61"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13;
46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science and Technology (UMIST
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                                                                                  Genome Research
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REFERENCE
AUTHORS
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BU122081
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BZ253924
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                                                                                                                                                                                                                                                                                                                            BASE COUNT
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                           DEFINITION
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                      BU122081 850 bp 1603146589F1 CSEQCHL17 Gallus gallus
                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
plate: 499 row: B column: 10
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 833)
Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn
Zhao, Gebregeorgis, B., Overton, L., Russell, D., Chen, D., Riggs, F., (
Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BZ253924 833 bp DNA linear GSS 15-OCT-2002
CH230-499B10.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished Other_GSSs: CH230-499B10.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Institute for Génomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Norway rat)
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      sequence.
                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                      GATGGCCTTAAGTTCCTCT
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                                                                                                                                             GATGGCCTTAAGTTCCTCT 192
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                                                                                                                                                                                                                          Conservative,
                                                                                                                                                                                                                                                                                                                        Pieter de Jong"
165 c 170 g
                                                                                                                                                                                                                                                                                                                                                             /clone lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
CHORI-230 Rat (BN/S8NHsd/MCW) BAC library produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Female"
/cell_type="B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="CH230-499B10"
                                                                                                                                                                                                                                             8.3%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                            229
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47;
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                      nRNA linear EST 25-NOV-2002 CDNA clone ChEST146b24 5', mRNA
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BU121203
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                                                                                                                                                            sequence.
BU121203
BU121203.1
EST.
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1 (bases 1 to 850)

1 (bases 1 to 850)

1 Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs

A Courr. Biol. 12 (22), 1965-1969 (2002)
Gallus gallus (chicken)
Gallus gallus (chicken)
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus
1 (bases 1 to 873)
1 (bases 1 to 873)
1 (bases 1 to 873)
1 (bases 1, Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E
                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
                                                                                                                                                                                                                                               BU121203 873
603003002F1 CSEQCHL17 Gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: Simon. Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simon Hubbard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12445392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone lib="CSECCHL17"
/clone lib="CSECCHL17"
/note="Organ: kidney + adrenal; Vector: pBluescript II
KS(+); Site 1: EcoRI; Site 2: Not1; Modification of
KS(+); Site 1: EcoRI; Site 2: Not1; Modification of
pBluescript II KS(+) [Stratagene] vector to accommodate
cDNA produced with the T-trimmed protocol (Construction of
uni-directionally cloned cDNA libraries from messenger RNA
for improved 3; end DNA sequencing by Glenn Fu, et al.
U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with
NotI and EcoRI. Ligate in double stranded adaptor
containing BsgI and BamHI sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [5'ggccgcgtgcagccccggatccgaaaaaaag]
[5'aattctttttttcggatccggggctgcacgc] "
197 c 246 g 208 t
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| lab_host="DH10B"
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clone="ChEST146b24"
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gallus
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47;
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      Burt, D.W., Bosch, E., and Hubbard, S.J.
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                                                                                                                                                                                                                                                                                                                                   Gallus gallus (chicken)
Gallus gallus
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                                                          Department of Biomolecular Sciences University of Manchester Institute
                                                                                                                                                                                 1 (bases 1 to 873)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, A Comprehensive Collection of Chicken cDNAs
                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 01612008930
Fax: 01612360409
                                                                                                     Contact: Simon Hubbard
                                                                                                                                                                                                                                                                                                                                                                                                  BU387613.1 GI:25895614
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University of Manchester Institute of Science and Technology (UMIST
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Box 88, Manchester,
l: 01612008930
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Conservative 0; Mismatches
                                                                                                                                                                Biol. 12 (22), 1965-1969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="CSEQCHL17"
/note="Organ: kidney + adrenal; Vector: pBluescript II
/note="Organ: kidney + site_2: Not1; Modification of
KS(+); Site_1: EcoRI; Site_2: Not1; Modification of
pBluescript II KS(+) [Stratagene] vector to accommodate
cDNA produced with the T-trimmed protocol (Construction of
uni-directionally cloned cDNA libraries from messenger RNA
for improved 3' end DNA sequencing by Glenn Fu, et al.
U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with
NotI and EcoRI. Ligate in double stranded adaptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     containing BsgI and BamHI sites [5'ggccgcgtgcagccccggatccgaaaaaa
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[5'aattctttttttcggatccggggctgcacgc]"
192 c 245 g 227 t
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/sex="Female"
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/lab_host="DH10B"
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'strain="Compton Line 151"
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                   M60 1QD, UK
                                                                                                                                                                    (2002)
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48;
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                                                            of Science and Technology (UMIST
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SOURCE
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BZ255847
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151
                 Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/bacpac/or ering_information.htm). BAC end
plate: 382 row: K column: 20
Seq primer: SP6
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19; Conserv
                                                                                                                                                                                                                                                                                       Contact: Shaying Zhao
Department of Eukaryotic Genomics
Department of Ercharyotic Research
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., Jong,P. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus
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BZ255847.1 GI:23961629
GSS.
Class: BAC ends
                                                                                                                                                                                                                                          Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                       Other_GSSs: CH230-382K20.TV
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCTCACGGAGTCTGGATT 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 873)
                                                                                                                                                                                                                                                                                                                                                                                                                                    BAC End Sequences from Library CHORI-230 MboI segment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9323 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
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/note="Organ: trunks; Vector: pBluescript II KS(+);
/note="Organ: trunks; Vector: pBluescript II KS(+);
Site_1: EcoRI; Site_2: Not1; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
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48;
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REFERENCE
AUTHORS
TITLE
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BF980523/c
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KEYWORDS
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Query Match
Best Local Similarity 100.
Matches 19; Conservative
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Best Local
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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BF980523.1
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                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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                                                                                                                                                                                                                                                                                                                                                                  quality sequence stop: 650.
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                                                                                     /tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="NH10B (phage_resistant)"
/clone_lib="NIH_MGC_88"
/note="Organ: small_incestine; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
a 194 c 230 g 239 t
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219 c 164 g
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/clone_lib="CHRI-230 Segment 2"
/clone="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
CHORI-230 Rat (BN/S8NHsd/MCW) BAC library produced by
                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4395785"
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/clone="CH230-382K20"
                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
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                    8.3%; Score 19;
100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Estimate of human gene number provided by using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
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GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                        genome. For more information, please thttp://www.genoscope.cns.fr/Tetraodon.
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/clone lib="G"
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217 c 195 g 293
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/mol_type="genomic DNA"
/db_xref="texon:99883"
/clone="254C04"
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DEFINITION **FOCUS**

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E 1 (bases 1 to 238)

Aizawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T., Carninci, P., Hanagaki, T., Hayatsu, N., Hiraoka, T., Hirozane, T., Hodoyama, Y., Imotani, K., Ishii, Y., Ich, M., Izawa, M., Kawai, J., Kojima, Y., Konno, H., Kusakabe, M., Matsuyama, T., Miyazaki, A., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Okazaki, Y., Okido, T., Owa, C., Sakai, C., Sakai, K., Sasaki, D., Sato, K., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tanaka, T., Toya, T., Watahiki, A., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshiki, A., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTs (Aizawa, K. et al. 2000)
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238 bp mRNA linear EST 29-NOV-200
BB562950 RIKEN full-length enriched, adult male heart Mus musculus
cDNA clone 1010001C13 5', mRNA sequence.
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High
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 152000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
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CC317416.1 GI:30711474
                  Unpublished
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                 Mus musculus
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1 324 c 197 g
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/clone lib="TAM32"
/note="Vector: pECBAC1; Site_1: EcoRI; Site_2:
/nam32 Female Chicken library - for library and
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/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
/clone="TAM32-27L22"
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|mol_type="genomic DNA"
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for Genome Exploration Research Group, RIKEN Genomic
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URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Nishlyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 286)
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
                                                                                                                       BB564795
BB564795.1 GI:11455687
                                                            Mus musculus
                                                                            Mus musculus (house mouse)
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RIKEN full-length enriched, adult male stomach Mus
cDNA clone 2200001P22 5', mRNA sequence.
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pBluescript KS(+) after bulk excision from Lambda FLC I."
a 73 c 50 g 46 t
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/dev_stage="adult"
/lab_host="BNN132"
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/db_xref="taxon:10090"
/clone="1010001C13"
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                                                                                18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
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                                          AAATTTTTGATGGCCTTA
                                                                              Conservative
                                                                                                                                                                                 85
                                                                                                                                                                           /note="Site_1: XhoI; Site_2: SstI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="stomach"
/dev_stage="adult"
/lab_host="SOLR"
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                                        53
                                                                       Score 18; Db iv,
Pred. No. 1.2e+02;
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186 CCTCCGTCCCTCCATATT 203
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Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosid
Spermatophyta; Magnollophyta; eudicotyledons; Trifolieae;
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Spermattoideae; Oryzaae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
18; Conserv
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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BE230315.1 GI:8956640
                                                                                                                               Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O., Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Gianinazzi-Pears
                                                                                                                                                                                                                                                                                                    Medicago truncatula (barrel medic)
                                                                                                                                                                                                                                                                                                                                                                                                             MtBC39B07F1 MtBC Medicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: myeun@sun20.asti.re.kr
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Suwon, Kyunggido,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Cytogenetics
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e,M.C., Shin,Y.C.,
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                                                                                                           and Gamas, P
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82 331 290 0307
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                                                                                       truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryza sativa
/mol_type="mRNA"
/cultivar="Milyang23"
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/lab_host="E. coli SOLR"
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'clone="99AS667"
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lone MtBC39B07 T3, mRNA
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                Department of Cytogenetics
National Inst. of Agri. Sci. and
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sun20_asti.re.kr.
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                                                                                                                                                                                                                                                                                       Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
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99AS575 Rice Seedling Lambda ZAPII (indica cultivar-group) cDNA clone
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http://sequence.toulouse.inra.fr/Mtruncatula.html).
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Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :
                                                                                                                                                                             Large-scale Sequencing 
Unpublished
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                                                                                                                                                           Contact: Eun M.Y.
                                                                                                                                                                                                                            Nahm, B.H.
                                                                                                                                                                                                                                                    Lee, M.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2/3 calcined Terragreen mix in the presence of onion root fragments colonized by the arbuscular mycorrhizal fungus Glomus intraradices (Schenck & Smith, isolate LPAB). The plants were watered every day and twice a week with a modified nutrient Long Ashton solution without phosphate but with a high level of nitrate. After 3 weeks RNA was extracted from whole root systems. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-zap XR vector from Stratagene and packaged using Gigapack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using ExAssit helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France). Note: EST may be of fungal origin."
                                                                                                                                                                                                                                               ., Shin,Y.C., Lee,T.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pBluescript pSK; Site 1: EcoRI; Site 2: /note="Vector: pBluescript pSK; Site 1: EcoRI; Site 2: XhoI; M. truncatula sterilised seeds were germinated for 72h at 25 C, before transplanting into a 1/3 Epoisses soil
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      intraradices"
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/clone="MtBC39B07"
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/cultivar="Jemalong"
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Pred. No.
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                                                                                                              and
                                                                                                                                                                                                                                               Jeong, S.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 weeks post inoculation with Glomus
                                                                                                              Tech,
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CDNA Library Oryza sativa
99AS575, mRNA sequence.
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                                                                                                                                                                                                                                               Kim, J.K.,
                                                                                                                                                                                                     Rice Seedling
                                                                                                                                                                                                                                                                                                                      Poaceae;
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                                                                                                                                                                                                                                               Eun, M.Y. and
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18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolieae;
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EST.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 706-542-4412
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220 Riverbend Road, Athens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESTs from seedling roots of Medicago truncatula after treatment with beta glucan elicitor preparation from Phytophthora sojae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: hahn@ccrc.uga.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Michael G. Hahn
/clone lib="MGHG"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
/note="Vector: pBluescript SK-; Site 2: EcoRI; Site 2:
/note="Vector: pBluescript SK-; Site 2: EcoRI; Site 2: Eco
                                                                                                                                                                                                                                                                  /clone="pMGHG-9J11"
/tlssue type="Roots from four day old seedlings"
/tlssue type="Roots after treatment with beta gluc
/dev stage="2 days after treatment with beta gluc
elicitor preparation from Phytophthora sojae"
/lab host="E. coli strain XLOLR"
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/mol_type="mRNA"
/cultivar="Milyang23"
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/mol_type="mRNA"
/cultivar="A17"
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/lab_host="E. coli SOLR"
/clone_lib="Rice Seedling Lambda ZAPII cDNA Library"
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/clone="99AS575"
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1.4e+02;
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Best Local
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                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 518)

Mitelaw, C. A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J. Maize Genomics Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PUEGJ78TD ZM_0.6_1.0_KB genomic survey sequence. CC407239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                             genomic survey
AZ700056
                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: TF
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
Contact: Cathy Whitelaw
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                        Mus musculus
                                                                                                     RPCI-23-223H8.TV RPCI-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9712 Medical Center Drive, Rockville, MD 20850,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC407239.1 GI:30887329
                                                                                                                   AZ700056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays
                                       Mus musculus (house mouse)
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1 68 c 95 g 177 t 2 others
                                                                                                                                                                                                                                                                                                /clone="ZMMBTa246M12"
/clone lib="ZM 0.6 1.0 KB"
/clone lib="ZM 0.6 1.0 KB"
/note="Vector: pCR4-TOFO; Site_1: EcoRI; 0.6-1.0 kb
/coT selected genomic DNA library"
104 c 109 g 118 t
                                                                                                                                                                                                                                                                                                                                                                                /strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                             Town
                                                                                                                                                                                                                                                                                                                                                                                                       organism="Zea mays"
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Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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1.4e+02;
hes 0;
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RPCI-23-223H8,
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AUTHORS
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CA390726
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                                                                                          AUTHORS
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EST.
 Mol. Vis.
22103460
12107410
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18; Conserv
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Class: BAC ends.
                                                                                                                                            Homo sapiens
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                          CA390726 548 bp mRNA linear E CS112h07.y1 Human Retinal pigment epithelium/choroid (Un-normalized, unamplified): cs Homo sapiens cDNA cl 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones availability, please contact Pieter de Jong
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC
page: http://www.tigr.org/tdb/bac_endse/bac_end_intro.html
Plate: 223 row: H column: 8
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,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M.,
and Fraser,C.M.
                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 548)
Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A.,
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
Expressed sequence tag analysis of human RPE/choroid for the NEIBank Project: Over 6000 non-redundant transcripts, novel genes
and splice variants
Mol. Vis. 8 (4), 205-220 (2002)
                                                                                                                                                                                                                                                                                             Homo sapiens (human)
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/rotes "Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
/notes "Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
EcoRI; Site 2: EcoRI; Female C57BL/6U mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBCe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).

103 c 98 g 212 t
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/strain="C57BL/6J"
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'clone="RPCI-23-223H8"
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Pred. No. 1.4
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1.4e+02;
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                                                                                                                                          JOURNAL
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1M0165J13F Mouse 10kb plasmid UUGCIM library Mus
clone UUGC1M0165J13 F, genomic survey sequence.
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                                                                                                                                                                                                        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
Mus musculus
                                                                                  University of Utah Genome University of Utah
                                                                                                                                                                         Mouse whole genome scaffolding with paired
                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 550)
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Plate: 112 row: h column: 07
Seq primer M13RP1 reverse primer (ABI).
Location/Qualifiers
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Section on Molecular Structure and Function
                                                                                                                     Contact: Robert B.
                                                                                                                                          Unpublished
                                                                                                                                                                                           and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCCTACTCACTGTCCTC 132
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301 496 0078
              801 585 5606
801 585 7177
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/note="Organ: Eye; Vector: pcMVSPORT6; Two different donor eyes (75-80 years old) yielded approximately 600 mg of dissected RPE/choroid tissue. This in turn yielded 340 ug of total RNA and 7 ug of mRNA. A directionally cloned cDNA library in the pcMVSPORT6 vector was constructed at Life Technologies (Rockville, MD; now part of Invitrogen Corp), essentially following the protocols of the SuperScript Plasmid System (Invitrogen Corp). The library code designation was cs. For this library, cDNA inserts were cloned into the NotI/Mul sites of the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
                                                     USA
ddunn@genetics.utah.edu
                                                                                                                                                        inserts
                                                                  Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="RPE/choroid"
/dev_stage="Adult"
/lab_host="EMDH10B"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="cs112h07"
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Rodentia;
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hes 0;
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                                                                                                                                                                             end reads
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                                                                    20 S. 2030 E.,
                                                                                                                                                                                                                                                                                                                                                                                                                            musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                              GSS 03-OCT-2000
                                                                                                                                                                                                                                                                                  Murinae; Mus.
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ORGANISM
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AW687310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 TTCTACTCAGAAATTTTT 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
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Location/Qualifiers
                                                                                                                         Medicago truncatula root
                                                                                                                                                                                                                                                                                                                                       AW687310.2 GI:11930471
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="UUGC1M0165J13"
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Insert Length: 10000 Std Error: Plate: 0165 row: J column: 13 Seq primer: CGTGTAAAACGACGGCCAGT Class: plasmid ends
                                                                                                                                                                                                                                              1 (bases 1 to 580)
Watson, B.S., Shin, H.-S., Lopez-Meyer, M., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W., M., G.D. and Paiva, N.L.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Medicago truncatula (barrel medic)
Medicago truncatula
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
On Noble Parkway, Ardmore, OK 73402, USA
                                                                                                              Unpublished
On Apr 14, 2000 this sequence version
Contact: Paiva NL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NF008C04RT1F1033 Developing root Medicago truncatula cDNA clone NF008C04RT 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with TA DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/Clome_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: pWp2ny, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Pred. No. 1.5e+0;
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TITLE
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ORIGIN
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AUTHORS
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AG242176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        391
                                                                                                                                                                                                                                            Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute The First Laboratory for Plant Gene Research; 2-6-7 Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan (B-mail:ssato@kazusa.or;)p, URL:http://www.kazusa.or.jp/en/plant/.Tel:81-438-52-3935(ex.2336), Fax:81-438-52-3934)
Location/Qualifiers
 l Similarity
                                                                                                                                                                                                                                                                                                                                                                                           Sato,S., Nakamura,Y. and Tabata,S. Lotus japonicus TAC End sequences Published Only in Database (2002) 2 (bases 1 to 589)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lotus japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lotus japonicus DNA, AG242176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: nlpaiva@noble.org
Theart Length: 738 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                              Sato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lotus japonicus
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ilarity 100.0%;
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                     /mol_type="genomic DNA"
/strain="Miyakojima MG-20"
/db_xref="taxon:34105"
/clone="LjT10d14_sfi"
/clone lib="genomic TAC library"
/note="VECTOR:PYLTAC7"
a 102 c 59 g 221 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-nodulated roots of plants grown in 1 mM nitrate medium. Samples were taken at four time points (approximately two days, one, two and six weeks post germination) representing early seedling growth to nitrogen limitation."

135 g 162 t
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/dev_stage="Pooled developmental"
/clone_lib="Developing_root"
/note="Vector: Lambda_Zap; Total RNA_was_extracted_from
                                                                                                                                                                                            /organism="Lotus japonicus"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Medicago truncatula"
/mol_type="mRNA"
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                                   7.9%;
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                Score 18; Pred. No.
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Pred. No.
 Mismatches
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 1.5e+02;
hes 0;
                                 DB 29;
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                                                                                                                                                                                                                                                                                                                    Kazusa DNA Research Institute, Research; 2-6-7
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genomic s
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                                 Length 589;
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CB934904/c
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McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvill,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson by Martin and Martin a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heterodera glycines
Heterodera glycines
Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
This library was generated by cloning cDNAs directionally into
Uni-ZAP(Stratagene) (T3 primer/EcoRI are at the 5'-end and T7/XhoI
are at the 3'-end). The library was excised [now in pBluescript
SK(+)] and normalized (Bonaldo et al 1996 Genome Research 6:791-806
). Library constructed by Thomas Baum (tbaum@iastate.edu), Iowa
State University, Plant Pathology Department and Jeff McDermott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (jpmcderm@iastate.edu).
Seq primer: T3 from Gibco
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Fax: 314 286 1810
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similar to
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                                                                                                                                                                                                   Similarity
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                                                                              TTTGTCCTCCACTTTCAC 226
                                                                                                                                                                                                                                                                                                                                                                        127
                                                                                                                                                            larity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    /Glone lib="Heterodera glycines egg"
/note="Vector: pBluescript SK+ (Stratagene); Site 1: XhoI;
/note="Vector: pBluescript SK+ (Stratagene); Site 1: XhoI;
Site 2: EcoRI; This library was generated by cloning cDNAs
directionally into Uni-ZAP(Stratagene) (T3 primer/EcoRI
are at the 5'-end and T7/XhoI are at the 3'-end). The
library was excised (now in pBluescript SK+)] and
normalized (Bonaldo et al 1996 Genome Research 6:791-806).
Library constructed by Thomas Baum (tbaum@iastate.edu),
Liowa State University, Plant Pathology Department and Jeff
                                                                                                                                                                                                                                                                                                                                                               McDermott (jpmcderm@iastate.edu)."
1 156 c 194 g 124 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:51029"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue_type="whole organism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Heterodera glycines"
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                                                                                                                                                            <u>,</u>
                                                                                                                                                            Score 18; DB 14; Pred. No. 1.5e+02; 0; Mismatches 0;
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                                                                                                                                                                                                                                          Length 601;
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VERSION
KEYWORDS
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AUTHORS
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CA922246/c
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KEYWORDS
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AF074623/c
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ORIGIN
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Matches
                                       ORGANISM
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Best Local Similarity
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CA922246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave,
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                             AF074623 Human fetal liver CDNA Ha0156, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VandenBosch, K., Endre, G., Silverstein Utterback, T., Cheung, F. and Fraser, C. The Medicago truncatula 6K unigene so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Medicago truncatula
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EST639964 MTUS Medicago truncatula
                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: kvandenb@cbs.umn.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: VandenBosch K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CA922246.1
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                                                      iomo sapiens (human)
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                                                                                                                                                                                                                                                             TCAGAAATTTTTGATGGC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R sequence name: MTUBY29TV
e information is available at: www.medicago.
[ primer: (gtA AtA CgA CtC ACt AtA ggg C).
Location/Qualifiers
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612 625 1738
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                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="MTUS"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."

135 c 86 g 197 t
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/dev_stage="various stages"
/lab_host="XLOLR"
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                                                                                            GI:6470442
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.one="MTUS-51C5"
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Pred. No.
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   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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library
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1.5e+02;
thes 0;
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JOURNAL COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beijing Institute of Radiation Medicine
27 Taiping Road, Beijing 100850, P.R.China
Tel: 0086-10-68159479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Yongtao Yu
Department of Hematology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expression profile analysis of a through large-scale sequencing
                                                                                                                                                                                                        Beijing Institute of Radiation Medicine
27 Taiping Road, Beijing 100850, P.R.Ch
                                                                                                                                                                                                                                   Contact: Yongtao Yu
Department of Hematology
                                                                                                                                                                                                                                                                                           and He, F
                                                                                                                                                                                                                                                                                                        Yu, Y
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 655)
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HA0156 Human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: yyt48@yahoo.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yu, Y.,
                                                                                                                                                                 Email: yyt48@yahoo.com
                                                                                                                                                                                Fax: 0086-10-68214653
                                                                                                                                                                                           Tel: 0086-10-68159479
                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                             Expression profile analysis of a human fetal liver cDNA library
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
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                           /clone_lib="Human fetal liver cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="fetal"
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/clone_lib="Human_fetal_liver_cDNA_library"
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/db_xref="taxon:9606"
/clone="Ha0156"
                                                      /dev_stage="fetal"
/lab_host="MC1061/P3"
                                                                                                                        organism="Homo sapiens"
                                                                                                                                                    ocation/Qualifiers
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Pred. No.
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Query Match

7.98;

DB 9;

Length 655;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute, The First Laboratory for Plant Gene Research; 2-6-7 Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan (B-mail:ssato@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/, Tel:81-438-52-3935[ex.2336], Fax:81-438-52-3934)
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                                                                                                                                       Zea mays
Zea mays
                                                                                                                                                                                                                        OGAHP24TC ZM2_0.7_1.5_KB genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sato,S., Nakamura,Y. and Tabata,S. Lotus japonicus TAC End sequences Published Only in Database (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AG242178 659 bp DNA linear GSS 12-DBC-20: Lotus japonicus DNA, clone:LjT10d15_sfi, genomic survey sequence. AG242178 AG242178.1 GI:26553015
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sato, S.
                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 665)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="LjT10d15 sfi"
/clone_lib="genomic TAC library"
/clone_"VECTOR:PYLTAC7"
/note="VECTOR:PYLTAC7"
116 c 74 g 242 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="Miyakojima MG-20"
/db_xref="taxon:34305"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Lotus japonicus"
mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 674)
Myler,P.J., Vogt,C., Munden,H., Robertson,L., Sisk,E., Faze
, Aggarwal,G., Nelson,S., Seyler,A., Worthey,E., Stuart,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                       Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                               Seattle Biomedical Research Institute
                                                                                                                                                                                                                                                                                                                                                                                              Other_GSSs: LB00548a.d_T7.1
Contact: Myler PJ
                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ragland, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leishmania major
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 301-838-0208
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                                                                                                                                                                                                                                                                                                         Email: mylerpj@sbri.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leishmania major
                                                                                                                                                                                                                                                                                                                         Tel: 206 284-8846
Fax: 206 284-0313
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/clone lib="ZM2 0.7 1.5 kB"
/note="Vector: pBCSK; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
a 116 c 108 g 189 t
/clome lib="Leishmania major Friedlin BAC Library"
/note="Vector: pCG270; Site 1: HindIII; Genomic DNA from
Leishmania major Friedlin in agarose blocks was partially
digested with HindIII, size selected, and ligated with
HindIII-digested pCG270 vector DNA. 10368 clones were
picked and arrayed in 384- and 96-will plates. Library
construction and arraying was carried out by ResGen
                                                                                                                                                                              /organism="Leishmania major"
/mol_type="genomic DNA"
/strain="Friedlin"
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/db_xref="taxon:4577"
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                                                                                                                              lab_host="E. coli GeneHogs +
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Medicago truncatula
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More information is available at:
Seq primer: (gtA AtA CgA CtC ACt I
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 704)
VandenBosch,K., Endre,G., Silverstein,K, Town,C.D., Van Aken,S.,
Utterback,T., Cheung,F. and Fraser,C.M.
The Medicago truncatula 6K unigene set: cDNA clones selected and
re-arrayed from various libraries
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CA922247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 612 624 2755
Fax: 612 625 1738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: VandenBosch K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: kvandenb@cbs.umn.edu
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                                                                                                                                              /clone lib="MTUS"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
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                                                                                                                                                                                                                                                                                                  /tissue_type="mixed tissues"
/dev_stage="various stages"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                    mol_type="mRNA"
/cultivar="A17"
                                                                                                                                                                                                                                                                                                                                                    db_xref="taxon:3880"
clone="MTUS-51C6"
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100.0%; Pr
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Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can

Clone distribution: MGC clone distribution information can
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="retinoblastoma"
/lab host="DH10B (phage-resistant)"
/clome_lb="NIH_MGC_16"
/clome_lib="NIH_MGC_16"
/clome_lib="NIH_MGC_16"
/clome_lib="NIH_MGC_16"
/clome_lib="NIH_MGC_16"
/clomed_into_EccRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC_Library."
25 a 176 c 206 g 200 t
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